

modified in attempts to achieve a more beneficial therapeutic profile. Examples of modified Type I IFNs are well known in the art (see Table 9), and are described in, for example U.S. Patent No. 6,323,006, in which cysteine-60 is substituted for tyrosine, U. S. Patent Nos. 4,737,462, 4,588,585, 5,545,723, and 6,127,332 where an IFN beta with a substitution of a variety of amino acids is described. Additionally, U.S. Patent Nos. 4,966,843, 5,376,567, 5,795,779 describe IFN alpha-61 and IFN-alpha-76. U.S. Patent Nos. 4,748,233 and 4,695,543 describe IFN alpha gx-1, whereas U.S. Patent No. 4,975,276 describes IFN alpha-54. In addition, U.S. Patent Nos. 4,695,623, 4,897,471, 5,661,009, and 5,541,293 all describe a consensus IFN alpha sequence to represent all variants known at the date of filing. While this list of Type I IFNs and variants thereof is in no way meant to be exhaustive, one of skill in the art will readily understand that the present invention encompasses IFN beta and IFN alpha molecules, derivatives, and variants known or to be discovered in the future.

Table 9. Interferon- $\alpha$  Isoforms.

$\alpha$ type	AA characteristic
1a	A <sup>114</sup>
1b	V <sup>114</sup>
2a	K <sup>23</sup> -H <sup>34</sup>
2b	R <sup>23</sup> -H <sup>34</sup>
2c	R <sup>23</sup> -R <sup>34</sup>
4a	A <sup>51</sup> -E <sup>114</sup>
4b	T <sup>51</sup> -V <sup>114</sup>
7a	M <sup>132</sup> -K <sup>159</sup> -G <sup>161</sup>
7b	M <sup>132</sup> -Q <sup>159</sup> -R <sup>161</sup>
7c	T <sup>132</sup> -K <sup>159</sup> -G <sup>161</sup>
8a	V <sup>98</sup> -L <sup>99</sup> -C <sup>100</sup> -D <sup>101</sup> -R <sup>161</sup>
8b	S <sup>98</sup> -C <sup>99</sup> -V <sup>100</sup> -M <sup>101</sup> -R <sup>161</sup>
8c	S <sup>98</sup> -C <sup>99</sup> -V <sup>100</sup> -M <sup>101</sup> -D <sup>161</sup> $\Delta$ (162-166)
10a	S <sup>8</sup> -L <sup>89</sup>
10b	T <sup>8</sup> -I <sup>89</sup>
14a	F <sup>152</sup> -Q <sup>159</sup> -R <sup>161</sup>
14b	F <sup>152</sup> -K <sup>159</sup> -G <sup>161</sup>
14c	L <sup>152</sup> -Q <sup>159</sup> -R <sup>161</sup>
17a	P <sup>34</sup> -S <sup>55</sup> -I <sup>161</sup>
17b	H <sup>34</sup> -S <sup>55</sup> -I <sup>161</sup>
17c	H <sup>34</sup> -S <sup>55</sup> -R <sup>161</sup>
17d	H <sup>34</sup> -P <sup>55</sup> -R <sup>161</sup>
21a	M <sup>96</sup>
21b	L <sup>96</sup>

Methods of expressing IFN in recombinant cells are well known in the art, and is easily accomplished using techniques described in, for example U.S. Patent No. 4,966,843, and in Sambrook et al. (2001, Molecular Cloning: A Laboratory Manual, Cold Spring Harbor Laboratory Press, New York) and Ausubel et al. (1997, Current Protocols in Molecular Biology, Green & Wiley, New York). Assays to determine the biological activity of a Type I IFN modified by the present invention will be well known to the skilled artisan. For example, the assay described in Rubinstein et al., (1981, Journal of Virology 37:755-758) is commonly used to determine the effect of an Type I IFN by measuring the cytopathic effects of viral infection on a population of cells. This method is only one of many known in the art for assaying the biological function of a Type IFN.

#### C. Factor VIIa

The present invention further encompasses a method for the remodeling and modification of Factor VII. The blood coagulation pathway is a complex reaction comprising many events. An intermediate event in this pathway is Factor VII, a proenzyme that participates in the extrinsic pathway of blood coagulation by converting (upon its activation to Factor VIIa) Factor X to Xa in the presence of tissue factor and calcium ions. Factor Xa in turn then converts prothrombin to thrombin in the presence of Factor Va, calcium ions and phospholipid. The activation of Factor X to Factor Xa is an event shared by both the intrinsic and extrinsic blood coagulation pathways, and therefore, Factor VIIa can be used for the treatment of patients with deficiencies or inhibitors of Factor VIII. There is also evidence to suggest that Factor VIIa may participate in the intrinsic pathway as well therefore increasing the prominence and importance of the role of Factor VII in blood coagulation.

Factor VII is a single-chain glycoprotein with a molecular weight of approximately 50 kDa. In this form, the factor circulates in the blood as an inactive zymogen. Activation of Factor VII to VIIa may be catalyzed by several different plasma proteases, such as Factor XIIIa. Activation of Factor VII results in the formation of a heavy chain and a light chain held together by at least one disulfide bond. Further, modified Factor VII molecules that cannot be converted to Factor VIIa have been described, and are useful as anti-coagulation remedies,

such as in the case of blood clots, thrombosis, and the like. Given the importance of Factor VII in the blood coagulation pathway, and its use as a treatment for both increased and decreased levels of coagulation, it follows that a molecule that has a longer biological half-life, increased potency, and in general, a therapeutic profile more similar to wild-type Factor VII as it is synthesized and secreted in the healthy human would be beneficial and useful as a treatment for blood coagulation disorders.

A remodeled Factor VII peptide may be administered to a patient selected from the group consisting of a hemophiliac patient having a bleeding episode, a patient having Hemophilia A, a patient with Hemophilia B, a patient having Hemophilia A, wherein the patient also has antibodies to Factor VIII, a patient having Hemophilia B, wherein the patient also has antibodies to Factor IX, a patient having liver cirrhosis, a cirrhotic patient having an orthotopic liver transplant, a cirrhotic patient having upper gastrointestinal bleeding, a patient having a bone marrow transplant, and a patient having a liver resection. Preferably, the patient is a human patient.

Factor VII has been cloned and sequenced, and the nucleic acid and amino acid sequences are presented herein as SEQ ID NO:7 and SEQ ID NO:8 (Figure 61A and 61B, respectively). The present invention should in no way be construed as limited to the Factor VII nucleic acid and amino acid sequences set forth herein. Variants of Factor VII are described in, for example, U.S. Patent Nos. 4,784,950 and 5,580,560, in which lysine-38, lysine-32, arginine--290, arginine-341, isoleucine-42, tyrosine-278, and tyrosine-332 is replaced by a variety of amino acids. Further, U.S. Patent Nos. 5,861,374, 6,039,944, 5,833,982, 5,788,965, 6,183,743, 5,997,864, and 5,817,788 describe Factor VII variants that are not cleaved to form Factor VIIa. The skilled artisan will recognize that the blood coagulation pathway and the role of Factor VII therein are well known, and therefore many variants, both naturally occurring and engineered, as described above, are included in the present invention.

Methods for the expression and to determine the activity of Factor VII are well known in the art, and are described in, for example, U.S. Patent No. 4,784,950. Briefly, expression of Factor VII, or variants thereof, can be accomplished in a variety of both prokaryotic and eukaryotic systems, including *E. coli*, CHO cells, BHK cells, insect cells using a baculovirus expression system, all of which are well known in the art.

Assays for the activity of a modified Factor VII prepared according to the methods of the present invention can be accomplished using methods well known in the art. As a non-limiting example, Quick et al. (Hemorrhagic Disease and Thrombosis, 2nd ed., Lea Febiger, Philadelphia, 1966), describes a one-stage clotting assay useful for determining the biological activity of a Factor VII molecule prepared according to the methods of the present invention.

#### D. Factor IX

The present invention further encompasses a method for remodeling and/or modifying Factor IX. As described above, Factor IX is vital in the blood coagulation cascade. A deficiency of Factor IX in the body characterizes a type of hemophilia (type B). Treatment of this disease is usually limited to intravenous transfusion of human plasma protein concentrates of Factor IX. However, in addition to the practical disadvantages of time and expense, transfusion of blood concentrates involves the risk of transmission of viral hepatitis, acquired immune deficiency syndrome or thromboembolic diseases to the recipient.

While Factor IX has demonstrated itself as an important and useful compound for therapeutic applications, present methods for the production of Factor IX from recombinant cells (U.S. Patent No. 4,770,999) results in a product with a rather short biological life, an inaccurate glycosylation pattern that could potentially lead to immunogenicity, loss of function, an increased need for both larger and more frequent doses in order to achieve the same effect, and the like.

A remodeled Factor IX peptide may be administered to a patient selected from the group consisting of a hemophiliac patient having a bleeding episode and also having Hemophilia B, a patient having Hemophilia B, a patient having Hemophilia B and having antibodies to Factor IX, a patient having liver cirrhosis, a cirrhotic patient having an orthotopic liver transplant, a cirrhotic patient having upper gastrointestinal bleeding, a patient having a bone marrow transplant, and a patient having a liver resection. A remodeled Factor IX peptide may also be administered to control and/or prevent hemorrhagic episodes in a patient having Hemophilia B, congenital Factor IX deficiency, or Christmas disease. A remodeled Factor IX peptide may also be administered to a patient to control and/or prevent hemorrhagic episodes in the patient during surgery. Preferably, the patient is a human patient.

The nucleic and amino acid sequences of Factor IX is set forth herein as SEQ ID NO:9 and SEQ ID NO:10 (Figure 62A and 62B, respectively). The present invention is in no way limited to the sequences set forth herein. Factor IX variants are well known in the art, as described in, for example, U.S. Patent Nos. 4,770,999, 5,521,070 in which a tyrosine is replaced by an alanine in the first position, U.S. Patent No. 6,037,452, in which Factor XI is linked to an alkylene oxide group, and U.S. Patent No. 6,046,380, in which the DNA encoding Factor IX is modified in at least one splice site. As demonstrated herein, variants of Factor IX are well known in the art, and the present disclosure encompasses those variants known or to be developed or discovered in the future.

Methods for determining the activity of a modified Factor IX prepared according to the methods of the present invention can be carried out using the methods described above, or additionally, using methods well known in the art, such as a one stage activated partial thromboplastin time assay as described in, for example, Biggs (1972, Human Blood Coagulation Haemostasis and Thrombosis (Ed. 1), Oxford, Blackwell, Scientific, pg. 614). Briefly, to assay the biological activity of a Factor IX molecule developed according to the methods of the present invention, the assay can be performed with equal volumes of activated partial thromboplastin reagent, Factor IX deficient plasma isolated from a patient with hemophilia B using sterile phlebotomy techniques well known in the art, and normal pooled plasma as standard, or the sample. In this assay, one unit of activity is defined as that amount present in one milliliter of normal pooled plasma. Further, an assay for biological activity based on the ability of Factor IX to reduce the clotting time of plasma from Factor IX-deficient patients to normal can be performed as described in, for example, Proctor and Rapaport (1961, Amer. J. Clin. Path. 36: 212).

#### E. FSH

The present invention further includes a method for remodeling and/or modifying FSH. Human reproductive function is controlled in part by a family of heterodimeric human glycoprotein hormones which have a common 92 amino acid glycoprotein alpha subunit, but differ in their hormone-specific beta subunits. The family includes follicle-stimulating hormone (FSH), luteinizing hormone (LH), thyrotropin or thyroid-stimulating hormone (TSH), and human chorionic gonadotropin (hCG). Human FSH and LH are used

therapeutically to regulate various aspects of metabolism pertinent to reproduction in the human female. For example, FSH partially purified from urine is used clinically to stimulate follicular maturation in anovulatory women with anovulatory syndrome or luteal phase deficiency. Luteinizing hormone (LH) and FSH are used in combination to stimulate the development of ovarian follicles for *in vitro* fertilization. The role of FSH in the reproductive cycle is sufficiently well-known to permit therapeutic use, but difficulties have been encountered due, in part, to the heterogeneity and impurity of the preparation from native sources. This heterogeneity is due to variations in glycosylation pattern.

FSH is a valuable tool in both *in vitro* fertilization and stimulation of fertilization *in vivo*, but as stated above, its clinical efficacy has been hampered by inconsistency in glycosylation of the protein. It therefore seems apparent that a method for remodeling FSH will be of great benefit to the reproductive sciences.

A remodeled FSH peptide may be administered to a patient selected from the group consisting of a patient undergoing intrauterine insemination (IUI), a patient undergoing *in vitro* fertilization (IVF), and an infertile patient. A remodeled FSH peptide may also be administered to induce or increase ovulation in a patient, to stimulate development of an ovarian follicle in a patient, to induce gametogenic follicle growth in a patient, to stimulate, induce or increase follicle development and subsequent ovulation in a patient, or to treat infertility in a patient. Preferably, the patient is a human female patient. A remodeled FSH peptide may also be administered to a patient having a pituitary deficiency or to a patient during puberty. Preferably this patient is a human male patient.

FSH has been cloned and sequenced, the nucleic and amino acid sequences of which are presented herein as SEQ ID NO:11, SEQ ID NO: 12, respectively (alpha subunit) and SEQ ID NO:13 and SEQ ID NO:14, respectively (beta subunit) (Figure 63A, 63B, 63C and 63D, respectively). The skilled artisan will readily appreciate that the present invention is not limited to the sequences depicted herein, as variants of FSH are well known in the art. As a non-limiting example, U.S. Patent No. 5,639,640 describes the beta subunit comprising two different amino acid sequences and U.S. Patent No. 5,338,835 describes a beta subunit comprising an additional amino acid sequence of approximately twenty-seven amino acids derived from the beta subunit of human chorionic gonadotropin. Therefore, the present

invention comprises FSH variants, both natural and engineered by the human hand, all well known in the art.

Methods to express FSH in cells, both prokaryotic and eukaryotic, are well known in the art and abundantly described in the literature (U.S. Patent Nos. 4,840,896, 4,923,805, 5,156,957). Further, methods for evaluating the biological activity of a remodeled FSH molecule of the present invention are well known in the art, and are described in, for example, U.S. Patent No. 4,589,402, in which methods for determining the effect of FSH on fertility, egg production, and pregnancy rates is described in both non-human primates and human subjects.

#### F. EPO

The present invention further comprises a method of remodeling and/or modifying EPO. EPO is an acidic glycoprotein of approximately 34 kDa and may occur in three natural forms: alpha, beta, and asialo. The alpha and beta forms differ slightly in carbohydrate components but have the same potency, biological activity and molecular weight. The asialo form is an alpha or beta form with the terminal sialic acid removed. EPO is present in very low concentrations in plasma when the body is in a healthy state wherein tissues receive sufficient oxygenation from the existing number of erythrocytes. This normal concentration is enough to stimulate replacement of red blood cells which are lost normally through aging. The amount of erythropoietin in the circulation is increased under conditions of hypoxia when oxygen transport by blood cells in the circulation is reduced. Hypoxia may be caused by loss of large amounts of blood through hemorrhage, destruction of red blood cells by over-exposure to radiation, reduction in oxygen intake due to high altitudes or prolonged unconsciousness, or various forms of anemia. Therefore EPO is a useful compound for replenishing red blood cells after radiation therapy, anemia, and other life-threatening conditions.

A remodeled EPO peptide may be administered to a patient selected from the group consisting of a patient having anemia, an anemic patient having chronic renal insufficiency, an anemic patient having end stage renal disease, an anemic patient undergoing dialysis, an anemic patient having chronic renal failure, an anemic Zidovudine-treated HIV infected patient, an anemic patient having non-myeloid cancer and undergoing chemotherapy, and an

anemic patient scheduled to undergo non-cardiac, non-vascular surgery. A remodeled EPO peptide may also be administered to a patient undergoing surgery to reduce the need for an allogenic blood transfusion. A remodeled EPO peptide may also be administered to a patient at increased risk for a perioperative blood transfusion with significant anticipated blood loss.

5 Preferably, the patient is a human patient.

In light of the importance of EPO in aiding in the recovery from a variety of diseases and disorders, the present invention is useful for the production of EPO with a natural, and therefore more effective saccharide component. EPO, as it is currently synthesized, lacks the full glycosylation complement, and must therefore be administered more frequently and in  
10 higher doses due to its short life in the body. The invention also provides for the production of PEGylated EPO molecules with greatly improved half-life compared with what might be achieved by maximizing desirable glycoforms.

EPO has been cloned and sequenced, and the nucleotide and amino acid sequences are present herein as SEQ ID NO:15 and SEQ ID NO:16, respectively (Figure 64A and 64B,  
15 respectively). It will be readily understood by one of skill in the art that the sequences set forth herein are only an example of the sequences encoding and comprising EPO. As an example, U.S. Patent No. 6,187,564 describes a fusion protein comprising the amino acid sequence of two or more EPO peptides, U.S. Patent Nos. 6,048,971 and 5,614,184 describe mutant EPO molecules having amino acid substitutions at positions 101, 103, 104, and 108.  
20 U.S. Patent No. 5,106,954 describes a truncated EPO molecule, and U.S. Patent No. 5,888,772 describes an EPO analog with substitutions at position 33, 139, and 166. Therefore, the skilled artisan will realize that the present invention encompasses EPO and EPO derivatives and variants as are well documented in the literature and art as a whole.

Additionally, methods of expressing EPO in a cell are well known in the art. As  
25 exemplified in U.S. Patent Nos. 4,703,008, 5,688,679, and 6,376,218, among others, EPO can be expressed in prokaryotic and eukaryotic expression systems. Methods for assaying the biological activity of EPO are equally well known in the art. As an example, the Krystal assay (Krystal, 1983, Exp. Hematol. 11:649-660) can be employed to determine the activity of EPO prepared according to the methods of the present invention. Briefly, the assay  
30 measures the effect of erythropoietin on intact mouse spleen cells. Mice are treated with phenylhydrazine to stimulate production of erythropoietin-responsive red blood cell

progenitor cells. After treatment, the spleens are removed, intact spleen cells are isolated and incubated with various amounts of wild-type erythropoietin or the erythropoietin proteins described herein. After an overnight incubation,  $^3\text{H}$ -thymidine is added and its incorporation into cellular DNA is measured. The amount of  $^3\text{H}$ -thymidine incorporation is indicative of erythropoietin-stimulated production of red blood cells via interaction of erythropoietin with its cellular receptor. The concentration of the erythropoietin protein of the present invention, as well as the concentration of wild-type erythropoietin, is quantified by competitive radioimmunoassay methods well known in the art. Specific activities are calculated as international units measured in the Krystal assay divided by micrograms as measured as immunoprecipitable protein by radioimmunoassay.

Several different mutated EPO's with different glycosylation patterns have been reported. Many have improved stimulation of reticulocytosis activity without effecting the half-life of the peptide in the blood stream of the animal. It is contemplated that mutated EPO peptides can be used in place of the native EPO peptides in any of the glycan remodeling, glycoPEGylation and/or glycoconjugation embodiments described herein. Preferred mutations of EPO are listed in the following table, but not limited to those listed in the table (see, for example, Chern et al., 1991, Eur. J. Biochem. 202:225-229; Grodberg et al., 1993, Eur. J. Biochem. 218:597-601; Burns et al., 2002, Blood 99:4400-4405; U.S. Patent No. 5,614,184; GenBank Accession No. AAN76993; O'Connell et al., 1992, J. Biol. Chem. 267:25010-25018; Elliott et al., 1984, Proc. Natl. Acad. Sci. U.S.A. 81:2708-2712; Biossel et al., 1993, J. Biol. Chem. 268:15983-15993). The most preferred mutations of EPO are Arg<sup>139</sup> to Ala<sup>139</sup>, Arg<sup>143</sup> to Ala<sup>143</sup> and Lys<sup>154</sup> to Ala<sup>154</sup>. The preferred native EPO from which to make these mutants is the 165 aa form, which is depicted in Fig. 65; however other native forms of EPO may also be used. Finally, the mutations described in Table 10 may be combined with each other and with other mutations to make EPO peptides that are useful in the present invention.

**Table 10.** Mutations of EPO.

Mutation	Citation	Notes
Arg <sup>139</sup> to Ala <sup>139</sup>	J. Biol. Chem. 269:22839 (1994)	Increased activity in bioassays of 120% to 150%.
Arg <sup>143</sup> to Ala <sup>143</sup>		Increased activity in bioassays than native

Lys <sup>154</sup> to Ala <sup>154</sup>	J. Biol. Chem. 269:22839 (1994)	EPO. Increased activity in bioassays of 120% to 150%.
Ser <sup>126</sup> to Met <sup>126</sup>		
Met <sup>54</sup> to Leu <sup>54</sup>	U.S. Patent No. 4,385,260	
Met <sup>54</sup> to Leu <sup>54</sup>	U.S. Patent No. 4,385,260	
Asn <sup>38</sup> to Gln <sup>38</sup>		
Δ1-30	Funakoshi et al., 1993, Biochem. Biophys. Res. Commun. 195:717-722.	Mutant isolated from hepatocellular carcinoma.
Ser <sup>131</sup> Leu <sup>132</sup> to Asn <sup>131</sup> Phe <sup>132</sup>	Genbank Accession No. AAD13964.	
Pro <sup>149</sup> to Gln <sup>149</sup>		
Gly <sup>101</sup> to Ala <sup>101</sup>	U.S. Patent No. 5,615,184 J. Biol. Chem. 269:22839 (1994)	Increased activity in bioassays of 120% to 150%.
Ser <sup>147</sup> to Ala <sup>147</sup> and/or Ile <sup>146</sup> to Ala <sup>146</sup>	Wen et al., 1994, J. Biol. Chem. 269:22839-22846.	Mutation results in increased bioactivity.
Ser <sup>126</sup> to Thr <sup>126</sup>	J. Biol. Chem. 267:25010 (1992)	

#### G. GM-CSF

The present invention encompasses a method for the modification of GM-CSF. GM-CSF is well known in the art as a cytokine produced by activated T-cells, macrophages, endothelial cells, and stromal fibroblasts. GM-CSF primarily acts on the bone marrow to increase the production of inflammatory leukocytes, and further functions as an endocrine hormone to initiate the replenishment of neutrophils consumed during inflammatory functions. Further GM-CSF is a macrophage-activating factor and promotes the differentiation of Lagerhans cells into dendritic cells. Like G-CSF, GM-CSF also has clinical applications in bone marrow replacement following chemotherapy.

While G-CSF has demonstrated itself as an important and useful compound for therapeutic applications, present methods for the production of G-CSF from recombinant cells results in a product with a rather short biological life, an inaccurate glycosylation pattern that could potentially lead to immunogenicity, loss of function, an increased need for both larger and more frequent doses in order to achieve the same effect, and the like.

A remodeled GM-CSF peptide may be administered to a patient selected from the group consisting of a patient having Acute Myelogenous Leukemia (AML) or acute non-lymphocytic leukemia (ANLL), a patient undergoing leukapheresis to collect hematopoietic progenitor cells from the peripheral blood, a patient undergoing transplantation of autologous peripheral blood progenitor cells, a non-Hodgkin's lymphoma (NHL) patient undergoing an autologous bone marrow transplant, a Hodgkin's disease patient undergoing an autologous bone marrow transplant, and an acute lymphoblastic leukemia (ALL) patient undergoing an autologous bone marrow transplant. A remodeled GM-CSF peptide may also be administered to a patient to accelerate myeloid engraftment, to shorten time to neutrophil recovery following chemotherapy, to mobilize hematopoietic progenitor cells into the peripheral blood for collection by leukapheresis, or to promote myeloid reconstitution after autologous or allogeneic bone marrow transplantation (BMT). A remodeled GM-CSF peptide may also be administered to a patient in which bone marrow transplantation has failed or in which myeloid engraftment is delayed. Preferably, the patient is a human patient.

GM-CSF has been isolated and cloned, the nucleic acid and amino acid sequences of which are presented as SEQ ID NO:17 and SEQ ID NO:18, respectively (Figure 66A and 66B, respectively). The present invention encompasses a method for modifying GM-CSF, particularly as it relates to the ability of GM-CSF to function as a potent and functional biological molecule. The skilled artisan, when equipped with the present disclosure and the teachings herein, will readily understand that the present invention provides compositions and methods for the modification of GM-CSF.

The present invention further encompasses GM-CSF variants, as well known in the art. As an example, but in no way meant to be limiting to the present invention, a GM-CSF variant has been described in WO 86/06358, where the protein is modified for an alternative quaternary structure. Further, U.S. Patent No. 6,287,557 describes a GM-CSF nucleic acid sequence ligated into the genome of a herpesvirus for gene therapy applications. Additionally, European Patent Publication No. 0288809 (corresponding to PCT Patent Publication No. WO 87/02060) reports a fusion protein comprising IL-2 and GM-CSF. The IL-2 sequence can be at either the N- or C-terminal end of the GM-CSF such that after acid cleavage of the fusion protein, GM-CSF having either N- or C-terminal sequence

modifications can be generated. Therefore, GM-CSF derivatives, mutants, and variants are well known in the art, and are encompassed within the methods of the present invention.

The expression and activity of a modified GM-CSF molecule of the present invention can be assayed using methods well known in the art, and as described in, for example, U.S.

5 Patent No. 4,810,643. As an example, activity can be measured using radio-labeled thymidine uptake assays. Briefly, human bone marrow from healthy donors is subjected to a density cut with Ficoll-Hypaque (1.077 g/ml, Pharmacia, Piscataway, NJ) and low density cells are suspended in Iscove's medium (GIBCO, La Jolla, CA) containing 10% fetal bovine serum, glutamine and antibiotics. About  $2 \times 10^4$  human bone marrow cells are incubated  
10 with either control medium or the GM-CSF or the present invention in 96-well flat bottom plates at about 37° C in 5% CO<sub>2</sub> in air for about 2 days. Cultures are then pulsed for about 4 hours with 0.5 µCi/well of <sup>3</sup>H-thymidine (New England Nuclear, Boston, Mass.) and uptake is measured as described in, for example, Ventua, et al.(1983, Blood 61:781). An increase in <sup>3</sup>H-thymidine incorporation into human bone marrow cells as compared to bone marrow cells  
15 treated with a control compound is an indication of a active and viable GM-CSF compound.

#### H. IFN-gamma

It is an object of the present invention to encompass a method of modifying and/or remodeling IFN-gamma. IFN-gamma, otherwise known as Type II interferon, in contrast to  
20 IFN alpha and IFN beta, is a homodimeric glycoprotein comprising two subunits of about 21-24 kDa. The size variation is due to variable glycosylation patterns, usually not replicated when reproduced recombinantly in various expression systems known in the art. IFN-gamma is a potent activator of macrophages, increases MHC class I molecule expression, and to a lesser extent, a MHC class II molecule stimulatory agent. Further, IFN-gamma promotes T-  
25 cell differentiation and isotype switching in B-cells. IFN-gamma is also well documented as a stimulator of neutrophils, NK cells, and antibody responses leading to phagocyte-mediated clearance. IFN-gamma has been proposed as a treatment to be used in conjunction with infection by intracellular pathogens, such as tuberculosis and leishmania, and also as an anti-proliferative therapeutic, useful in conditions with abnormal cell proliferation as a hallmark,  
30 such as various cancers and other neoplasias.

IFN-gamma has demonstrated potent immunological activity, but due to variations in glycosylation from systems currently used to express IFN-gamma, the potency, efficacy, biological half-life, and other important factors of a therapeutic have been variable at best. The present invention encompasses methods to correct this crucial defect.

5 A remodeled interferon-gamma peptide may be administered to a patient selected from the group consisting of a patient having chronic granulomatous disease, a patient having malignant osteopetrosis, a patient having pulmonary fibrosis, a patient having tuberculosis, a patient having *Cryptococcal* meningitis, and a patient having pulmonary *Mycobacterium avium* complex (MAC) infection. Preferably, the patient is a human patient.

10 The nucleotide and amino acid sequences of IFN-gamma are presented herein as SEQ ID NO:19 and SEQ ID NO:20, respectively (Figure 67A and 67B, respectively). It will be readily understood that the sequences set forth herein are in no way limiting to the present invention. In contrast, variants, derivatives, and mutants of IFN-gamma are well known to the skilled artisan. As an example, U.S. Patent No. 6,083,724 describes a recombinant avian  
15 IFN-gamma and U.S. Patent No. 5,770,191 describes C-terminus variants of human IFN-gamma. In addition, U.S. Patent No. 4,758,656 describes novel IFN-gamma derivatives, and methods of synthesizing them in various expression systems. Therefore, the present invention is not limited to the sequences of IFN-gamma disclosed elsewhere herein, but encompasses all derivatives, variants, muteins, and the like well known in the art.

20 Expression systems for IFN-gamma are equally well known in the art, and include prokaryotic and eukaryotic systems, as well as plant and insect cell preparations, methods of which are known to the skilled artisan. As an example, U.S. Patent No. 4,758,656 describes a system for expressing IFN-gamma derivatives in *E. coli*, whereas U.S. Patent No. 4,889,803 describes an expression system employing Chinese hamster ovary cells and an SV40  
25 promoter.

Assays for the biological activity of a remodeled IFN-gamma prepared according to the methods disclosed herein will be well known to one of skill in the art. Biological assays for IFN-gamma expression can be found in, for example, U.S. Patent No. 5,807,744. Briefly, IFN-gamma is added to cultures of CD34<sup>++</sup>CD38<sup>-</sup> cells (100 cells per well) stimulated by  
30 cytokine combinations to induce proliferation of CD34<sup>++</sup>CD38<sup>-</sup> cells, such as IL-3, c-kit ligand and either IL-1, IL-6 or G-CSF. Cell proliferation, and generation of secondary

colony forming cells will be profoundly inhibited in a dose dependent way, with near complete inhibition occurring at 5000 U/milliliter of IFN-gamma. As a confirmatory test to the inhibitory effect of IFN-gamma, addition of IFN-gamma antibodies can be performed as a control.

#### I. alpha-Protease inhibitor ( $\alpha$ -antitrypsin)

The present invention further includes a method for the remodeling of alpha-protease inhibitor (A-1-PI,  $\alpha$ -1-antitrypsin or  $\alpha$ -1-trypsin inhibitor), also known as alpha-antitrypsin. A-1-PI is a glycoprotein having molecular weight of 53 kDa. A-1-PI plays a role in  
0 controlling tissue destruction by endogenous serine proteases, and is the most pronounced serine protease inhibitor in blood plasma. In particular, A-1-PI inhibits various elastases including neutrophil elastase. Elastase is a protease which breaks down tissues, and can be particularly problematic when its activity is unregulated in lung tissue. This protease functions by breaking down foreign proteins. However, when API is not present in sufficient  
15 quantities to regulate elastase activity, the elastase breaks down lung tissue. In time, this imbalance results in chronic lung tissue damage and emphysema. In fact, a genetic deficiency of A-1-PI has been shown to be associated with premature development of pulmonary emphysema. A-1-PI replenishment has been successfully used for treatment of this form of emphysema. Further, a deficiency of A-1-PI may also contribute to the  
20 aggravation of other diseases such as cystic fibrosis and arthritis, where leukocytes move in to the lungs or joints to fight infection.

Therefore, A-1-PI could conceivably be used to treat diseases where an imbalance between inhibitor and protease(s), especially neutrophil elastase, is causing progression of a disease state. Antiviral activity has also been attributed to A-1-PI. In light of this, it logically  
25 follows that the present invention is useful for the production of A-1-PI that is safe, effective, and potent in the ever changing atmosphere of the lungs.

A remodeled A-1-PI peptide may be administered to a patient selected from the group consisting of a patient having congenital alpha-1-antitrypsin deficiency and emphysema, a patient having cystic fibrosis, and a patient having pulmonary fibrosis. Preferably, the patient  
30 is a human patient.

A-1-PI has been cloned and sequenced, and is set forth in SEQ ID NO:21 and SEQ ID NO:22 (Figure 68A and 68B, respectively). As is understood by one of skill in the art, natural and engineered variants of A-1-PI exist, and are encompassed in the present invention. As an example, U.S. Patent No. 5,723,316 describes A-1-PI derivatives having amino acid substitutions at positions 356-361 and further comprises an N-terminal extension of approximately three amino acids. U. S. Patent No. 5,674,708 describes A-1-PI analogs with amino acid substitutions at position 358 in the primary amino acid sequence. The skilled artisan will readily realize that the present invention encompasses A-1-PI variants, derivatives, and mutants known or to be discovered.

Methods for the expression and determination of activity of a remodeled A-1-PI produced according to the methods of the present invention are well known in the art, and are described in, for example, U.S. Patent No. 5,674,708 and U.S. Patent No. 5,723,316. Briefly, biological activity can be determined using assays for antichymotrypsin activity by measuring the inhibition of the chymotrypsin-catalyzed hydrolysis of substrate N-suc-Ala--Ala--Pro--Phe-p-nitroanilide (0.1 ml of a 10 mM solution in 90% DMSO), as described in, for example, DelMar et al. (1979, Anal. Biochem. 99: 316). A typical chymotrypsin assay contains, in 1.0 milliliters: 100 mM Tris-Cl buffer, pH 8.3, 0.005% (v/v) Triton X-100, bovine pancreatic chymotrypsin (18 kmmol) and A-1-PI of the present invention. The assay mixture is pre-incubated at room temperature for 5 minutes, substrate (0.01 ml of a 10 mM solution in 90% DMSO) is added and remaining chymotrypsin activity is determined by the rate of change in absorbance at 410nm caused by the release of p-nitroaniline. Measurements of optical absorbance are conducted at 25° C using a spectrophotometer fitted with a temperature controlled sample compartment.

#### J. Glucocerebrosidase

The invention described herein further includes a method for the modification of glucocerebrosidase. Glucocerebrosidase is a lysosomal glycoprotein enzyme which catalyzes the hydrolysis of the glycolipid glucocerebroside to glucose and ceramide. Variants of glucocerebrosidase are sold commercially as Cerezyme™ and Ceredase™, and is an approved therapeutic for the treatment of Gaucher disease. Ceredase™ is a placental derived form of glucocerebrosidase with complete N-linked structures. Cerezyme™ is a recombinant

variant of glucocerebrosidase which is 497 amino acids in length and is expressed in CHO cells. The 4 N-linked glycans of Cerezyme have been modified to terminate in the trimannose core.

5 Glucocerebrosidase is presently produced in recombinant mammalian cell cultures, and therefore reflects the glycosylation patterns of those cells, usually rodent cells such as Chinese hamster ovary cells or baby hamster kidney cells, which differ drastically from those of human glycosylation patterns, leading to, among other things, immunogenicity and lack of potency.

10 A remodeled glucocerebrosidase peptide may be administered to a patient selected from the group consisting of a patient having a lysosomal storage disease, a patient having a glucocerebrosidase deficiency, and a patient having Gaucher disease. Preferably, the patient is a human patient.

The nucleic acid and amino acid sequences of glucocerebrosidase are set forth herein as SEQ ID NO:23 and 24 (Figure 69A and 69B, respectively). However, as will be  
15 appreciated by the skilled artisan, the sequences represented herein are prototypical sequences, and do not limit the invention. In fact, variants of glucocerebrosidase are well known, and are described in, for example, U.S. Patent 6,015,703 describes enhanced production of glucocerebrosidase analogs and variants thereof. Further, U.S. Patent No. 6,087,131 describes the cloning and sequencing of yet another glucocerebrosidase variant. It  
20 is the intention of the present invention to encompass these and other derivatives, variants, and mutants known or to be discovered in the future.

Methods for the expression of glucocerebrosidase are well known in the art using standard techniques, and are described in detail in, for example, U.S. Patent No. 6,015,703. Assays for the biological efficacy of a glucocerebrosidase molecule prepared according to the  
25 methods of the present invention are similarly well known in the art, and a mouse Gaucher disease model for evaluation and use of a glucocerebrosidase therapeutic is described in, for example, Marshall et al. (2002, Mol. Ther. 6:179).

#### K. TPA

30 The present invention further encompasses a method for the remodeling of tissue-type activator (TPA). TPA activates plasminogen to form plasmin which dissolves fibrin, the

main component of the protein substrate of the thrombus. TPA preparations were developed as a thrombolytic agents having a very high selectivity toward the thrombus in the thrombolytic treatment for thrombosis which causes myocardial infarction and cerebral infarction.

5 Further, various modified TPA's have been produced by genetic engineering for the purpose of obtaining higher affinity to fibrin and longer half-life in blood than that of natural TPA. TPA's are proteins that are generally extremely difficult to solubilize in water. In particular, the modified TPA's are more difficult to solubilize in water than natural TPA, making very difficult the preparation of modified TPA's. Modified TPA's are thus difficult to  
10 dissolve in water at the time of the administration to a patient. However, the modified TPA's have various advantages, such as increased affinity for fibrin and longer half-life in blood. It is the object of the present invention to increase the solubility of modified TPA's.

A remodeled TPA peptide may be administered to a patient selected from the group consisting of a patient suffering from an acute myocardial infarction and a patient suffering  
15 from an acute ischemic stroke. A remodeled TPA peptide may also be administered to a patient to improve ventricular function following an acute myocardial infarction, to reduce the incidence of congestive heart failure following an acute myocardial infarction, or to reduce mortality associated with acute myocardial infarction. A remodeled TPA peptide may also be administered to a patient to improve neurological recovery following an acute  
20 ischemic stroke or to reduce the incidence of disability or paralysis following an acute ischemic stroke. Preferably, the patient is a human patient.

The nucleic and amino acid sequences of TPA are set forth herein as SEQ ID NO:25 and SEQ ID NO:26, respectively (Figure 70A and 70B, respectively). As described above, variants of TPA have been constructed and used in therapeutic applications. For example,  
25 U.S. Patent 5,770,425 described TPA variants in which some of all of the fibrin domain has been deleted. Further, U.S. Patent 5,736,134 describes TPA in which modifications to the amino acid at position 276 are disclosed. The skilled artisan, when equipped with the present disclosure and the teachings herein, will readily realize that the present invention comprises the TPA sequences set forth herein, as well as those variants well known to one versed in the  
30 literature.

The expression of TPA from a nucleic acid sequence encoding the same is well known in the art, and is described, in detail, in, for example, U.S. Patent No. 5,753,486. Assays for determining the biological properties of a TPA molecule prepared according to the methods of the present invention are similarly well known in the art. Briefly, a TPA

5 molecule synthesized as disclosed elsewhere herein can be assayed for their ability to lyse fibrin in the presence of saturating concentrations of plasminogen, according to the method of Carlsen et al. (1988, Anal. Biochem. 168: 428 ). The *in vitro* clot lysis assay measures the activity of tissue-type activators by turbidimetry using a microcentrifugal analyzer. A mixture of thrombin and TPA is centrifuged into a mixture of fibrinogen and plasminogen to

10 initiate clot formation and subsequent clot dissolution. The resultant profile of absorbance versus time is analyzed to determine the assay endpoint. Activities of the TPA variants are compared to a standard curve of TPA. The buffer used throughout the assay is 0.06M sodium phosphate, pH 7.4 containing 0.01% (v/v) TWEEN 80 and 0.01% (w/v) sodium azide. Human thrombin is at a concentration of about 33 units/ml. Fibrinogen (at 2.0 mg/ml

15 clottable protein) is chilled on wet ice to precipitate fibronectin and then gravity filtered. Glu-plasminogen is at a concentration of 1 mg/ml. The analyzer chamber temperature is set at 37° C. The loader is set to dispense 20 microliters of TPA (about 500 nanograms/milliliter to about 1.5 micrograms per milliliter) as the sample for the standard curve, or 20 microliters of variant TPAs at a concentration to cause lysis within the range of the standard curve.

20 Twenty microliters of thrombin as the secondary reagent, and 200 microliters of a 50:1 (v/v) fibrinogen: plasminogen mixture as the primary reagent. The absorbance/time program is used with a 5 min incubation time, 340-nanometer-filter and 90 second interval readings.

#### L. IL-2

25 The present invention further encompasses a method for the remodeling and modification of IL-2. IL-2 is the main growth factor of T lymphocytes and increases the humoral and cellular immune responses by stimulating cytotoxic CD8 T cells and NK cells. IL-2 is therefore crucial in the defense mechanisms against tumors and viral infections. IL-2 is also used in therapy against metastatic melanoma and renal adenocarcinoma, and has been

30 used in clinical trials in many forms of cancer. Further, IL-2 has also been used in HIV infected patients where it leads to a significant increase in CD4 counts.

Given the success IL-2 has demonstrated in the management and treatment of life-threatening diseases such as various cancers and AIDS, it follows that the methods of the present invention would be useful for developing an IL-2 molecule that has a longer biological half-life, increased potency, and in general, a therapeutic profile more similar to wild-type IL-2 as it is synthesized and secreted in the healthy human.

A remodeled IL-2 peptide may be administered to a patient selected from the group consisting of a patient having metastatic renal cell carcinoma, a patient having metastatic melanoma, a patient having ovarian cancer, a patient having Acute Myelogenous Leukemia (AML), a patient having non-Hodgkin's lymphoma (NHL), a patient infected with HIV, and a patient infected with Hepatitis C. A remodeled IL-2 peptide may also be useful for administration to a patient as a cancer vaccine adjuvant. Preferably, the patient is a human patient.

IL-2 has been cloned and sequenced, and the nucleic acid and amino acid sequences are presented herein as SEQ ID NO:27 and SEQ ID NO:28 (Figure 71A and 71B, respectively). The present invention should in no way be construed as limited to the IL-2 nucleic acid and amino acid sequences set forth herein. Variants of IL-2 are described in, for example, U.S. Patent No. 6,348,193, in which the asparagine at position 88 is substituted for arginine, and in U.S. Patent No. 5,206,344, in which a polymer comprising IL-2 variants with various amino acid substitutions is described. The present invention encompasses these IL-2 variants and others well known in the art.

Methods for the expression and to determine the activity of IL-2 are well known in the art, and are described in, for example, U.S. Patent No. 5,417,970. Briefly, expression of IL-2, or variants thereof, can be accomplished in a variety of both prokaryotic and eukaryotic systems, including *E. coli*, CHO cells, BHK cells, insect cells using a baculovirus expression system, all of which are well known in the art.

Assays for the activity of a modified IL-2 prepared according to the methods of the present invention can proceed as follows. Peripheral blood lymphocytes can be separated from the erythrocytes and granulocytes by centrifuging on a Ficoll-Hypaque (Pharmacia, Piscataway, NJ) gradient by the method described in, for example, A. Boyum et al. (Methods in Enzymology, 1984, Vol. 108, page 88, Academic Press, Inc.). Lymphocytes are subsequently washed about three times in culture medium consisted of RPMI 1640 (Gibco-

BRL, La Jolla, CA) plus 10% AB human serum (CTS Purpan, Toulouse, France) inactivated by heat (1 hour at 56° C), 2 mM sodium pyruvate, 5 mM HEPES, 4 mM L-glutamine, 100 U/ml penicillin, 100 µg/ml streptomycin and 0.25 µg/ml amphotericin B (complete medium). Adhesive cells (monocytes and macrophages) are eliminated by adhesion to plastic and the  
5 remainder of the cells are suspended in complete medium at a concentration of about 5 to 10 X10<sup>5</sup> cells per milliliter and seeded in culture flasks at a density of about 1-2 X 10<sup>5</sup> cells per square centimeter. Flasks are then incubated at 37° C in a 5% CO<sub>2</sub> atmosphere for about 1 hour, after which the non-adhesive lymphocytes are recovered by aspiration after gentle agitation of the culture flasks.

10 Non-adhesive lymphocytes are washed once and cultivated at a concentration of about 10<sup>5</sup> cells per milliliter in complete medium in the presence of the IL-2 of the present invention for about 48 hours in an incubator as described above. The cells are then washed once.

The cytotoxic activity of the cells is evaluated after about 4 hours of contact with  
15 target cells of the human T lymphoid line C8166-45/C63 (HT1 cells) resistant to NK cell cytotoxicity, as described by Salahuddin et al. (1983, Virology 129: 51-64; 1984, Science: 223, 703-707). 6 X 10<sup>5</sup> HT1 cells are radio-tagged with about 200 µCi of <sup>51</sup>Cr (sodium chromate, Amersham, Arlington Heights, IL) at 37° C for about 1 hour in complete medium without serum, and then washed several times. The target cells and effective cells are  
20 distributed in round-bottomed microtitration plates with varying ratios of effective cells to target cells (50:1, 10:1, 1:1). The microtitration plates are centrifuged and, after incubation as described above, the supernatant from each well is recovered and the radioactivity is measured using a gamma counter. Cytotoxicity is determined from the quantity of <sup>51</sup>Cr released by dead target cells. Non-specific cytotoxicity is determined from the amount of  
25 radioactivity spontaneously released from the target cells in the absence of effective cells.

The present method is just one of many well known in the art for measuring the cytotoxicity of effector cells, and is should not be construed as limiting to the present invention.

### M. Factor VIII

The invention further encompasses a method for the remodeling and modification of Factor VIII. As described earlier for Factor VII and Factor IX, Factor VIII is a critical component of the blood coagulation pathway. Human Factor VIII, (antihemophilic factor; FVIII:C) is a human plasma protein consisting of 2 peptides (light chain molecular weight of 80 kDa and heavy chain molecular weight variable from 90 to 220 kDa, depending on glycosylation state). It is an essential cofactor in the coagulation pathway and is required for the conversion of Factor X into its active form (Factor Xa). Factor VIII circulates in plasma as a non-covalent complex with von Willibrand Factor (aka FVIII:RP), a dimer of a 2050 aa peptide (See, U.S. Patent No. 6,307,032). Blood concentrations of Factor VIII below 20% of normal cause a bleeding disorder designated hemophilia A. Factor VIII blood levels less than 1% result in a severe bleeding disorder, with spontaneous joint bleeding being the most common symptom.

Similar to other blood coagulation factors, Factor VIII is a therapeutic with a great deal of potential for the treatment of various bleeding disorders, such as hemophilia A and hemophilia B. Due to the glycosylation of the heavy chain, current methods for the preparation of Factor VIII from recombinant cells results in a product that is not as effective as natural Factor VIII. Purification methods from human plasma result in a crude composition that is less effective and more difficult to prepare than recombinant Factor VIII. The current invention seeks to improve this situation.

A remodeled Factor VIII peptide may be administered to a patient selected from the group consisting of a patient having von Willebrand's disease, a patient having Hemophilia A, a patient having Factor VIII:C deficiency, a patient having fibrinogen deficiency, a patient having Factor XIII deficiency, and a patient having acquired Factor VIII inhibitors (acquired hemophilia). A remodeled Factor VIII peptide may also be administered to a patient to prevent, treat or control bleeding or hemorrhagic episodes. Preferably, the patient is a human patient.

The nucleic acid and amino acid sequences of Factor VIII are presented herein as SEQ ID NO:29 and SEQ ID NO:30, respectively (Figure 72A and 72B, respectively). The art is rife with variants of Factor VIII, as described in, for example, U.S. Patent No. 5,668,108, in which the aspartic acid at position 1241 is replaced by a glutamic acid with the

accompanying nucleic acid changes as well. U.S. Patent No. 5,149,637 describes a Factor VIII variants comprising the C-terminal fraction, either glycosylated or unglycosylated, and U.S. Patent No. 5,661,008 describes a Factor VIII variant comprising amino acids 1-740 linked to amino acids 1649 to 2332 by at least 3 amino acid residues. Therefore, variants, derivatives, modifications and complexes of Factor VIII are well known in the art, and are encompassed in the present invention.

Expression systems for the production of Factor VIII are well known in the art, and include prokaryotic and eukaryotic cells, as exemplified in U.S. Patent Nos. 5,633,150, 5,804,420, and 5,422,250.

To determine the biological activity of a Factor VIII molecule synthesized according to the methods of the present invention, the skilled artisan will recognize that the assays described herein for the evaluation of Factor VII and Factor IX are applicable to Factor VIII.

#### N. Urokinase

The present invention also includes a method for the remodeling and/or modification of urokinase. Urokinase is a serine protease which activates plasminogen to plasmin. The protein is synthesized in a variety of tissues including endothelium and kidney, and is excreted in trace amounts into urine. Purified urokinase exists in two active forms, a high molecular weight form (HUK; approximately 50 kDa) and a low molecular weight form (LUK; approximately 30 kDa). LUK has been shown to be derived from HUK by a proteolysis after lysine 135, releasing the first 135 amino acids from HUK. Conventional wisdom has held that HUK or LUK must be converted to proteolytically active forms by the proteolytic hydrolysis of a single chain precursor, also termed prourokinase, between lysine 158 and isoleucine 159 to generate a two-chain activated form (which continues to correspond to either HUK or LUK). The proteolytically active urokinase species resulting from this hydrolytic clip contains two amino acid chains held together by a single disulfide bond. The two chains formed by the activation clip are termed the A or A<sub>1</sub> chains (HUK or LUK, respectively), and the B chain comprising the protease domain of the molecule.

Urokinase has been shown to be an effective thrombolytic agent. However, since it is produced naturally in trace quantities the cost of the enzyme is high for an effective dosage. Urokinase has been produced in recombinant cell culture, and DNA encoding urokinase is

known together with suitable vectors and host microorganisms. Present compositions comprising urokinase and methods for producing urokinase recombinantly are hampered by a product that has deficient glycosylation patterns, and given the complex proteolytic cleavage events surrounding the activation of urokinase, this aberrant glycosylation leads to a less effective and less potent product.

A remodeled urokinase peptide may be administered to a patient selected from the group consisting of a patient having an embolism, a patient having an acute massive pulmonary embolism, and a patient having coronary artery thrombosis. Preferably, the patient is a human patient. A remodeled urokinase peptide may also be used to restore patency to an intravenous catheter, including a central venous catheter obstructed by clotted blood or fibrin.

The sequence of the nucleotides encoding the primary amino acid chain of urokinase are depicted in SEQ ID NO:33 and SEQ ID NO:34 (Figure 73A and 73B, respectively). Variants of urokinase are well known in the art, and therefore the present invention is not limited to the sequences set forth herein. In fact, the skilled artisan will readily realize that urokinase variants described in, for example U.S. Patent Nos. 5,219,569, 5,648,253, and 4,892,826, exist as functional moieties, and are therefore encompassed in the present invention.

The expression and evaluation of a urokinase molecule prepared according to the methods of the present invention are similarly well known in the art. As a non-limiting example, the expression of urokinase in various systems is detailed in U.S. Patent No. 5,219,569. An assay for determining the activity and functionality of a urokinase prepared in accordance to the methods set forth herein are described throughout the literature, and are similar to assays for other plasminogen and fibrin related assays described elsewhere throughout. One example of an assay to determine the activity of an urokinase molecule synthesized as described herein can be as described in, for example, Ploug, et al. (1957, Biochim. Biophys. Acta 24: 278-282), using fibrin plates comprising 1.25% agarose, 4.1 mg/ml human fibrinogen, 0.3 units/ml of thrombin and 0.5 µg/ml of soybean trypsin inhibitor.

### O. Human DNase

The present invention further encompasses a method for the remodeling and/or modification of recombinant human DNase. Human DNase I has been tested as a therapeutic agent and was shown to diminish the viscosity of cystic fibrosis mucus *in vitro*. It has been determined that purulent mucus contains about 10-13 mg/ml of DNA, an ionic polymer predicted to affect the rheologic properties of airway fluids. Accordingly, bovine pancreatic DNase I, an enzyme that degrades DNA, was tested as a mucolytic agent many years ago but did not enter clinical practice, because of side effects induced by antigenicity and/or contaminating proteases. Recombinant human DNase is currently used as a therapeutic agent to alleviate the symptoms of diseases such as cystic fibrosis.

A remodeled rDNase peptide may be administered to a patient having cystic fibrosis. A remodeled rDNase peptide may also be administered to a cystic fibrosis patient to improve pulmonary function. Preferably, the patient is a human patient.

Similar to DNase derived from bovine sources, recombinant human DNase poses some problems, mostly due to lowered efficacy due to improper glycosylation imparted by mammalian expression systems currently in use. The present invention describes a method for remodeling DNase, leading to increased efficacy and better therapeutic results.

The nucleotide and amino acid sequences of human DNase are presented herein as SEQ ID NO:39 and SEQ ID NO:40 (Figure 74A and 74B, respectively). Variants of the peptide comprising DNase are well known in the art. As an example, U.S. Patent No. 6,348,343 describes a human DNase with multiple amino acid substitutions throughout the primary structure. Additionally, U.S. Patent No. 6,391,607 describes a hyperactive variant of DNase with multiple amino acid substitutions at positions 9, 14, 74, 75, and 205. The present examples, and others well known in the art or to be discovered in the future are encompassed in the present invention.

Expression systems for producing a DNase peptide are well known to the skilled artisan, and have been described in prokaryotic and eukaryotic systems. For example, PCT Patent Publication No. WO 90/07572 describes these methods in considerable detail.

Assays to determine the biological activity of a DNase molecule developed according to the methods of the present invention are well known in the art. As an example, but in no way meant to be limiting to the present invention, an assay to determine the DNA-hydrolytic

activity of human DNase I is presented herein. Briefly, two different plasmid digestion assays are used. The first assay ("supercoiled DNA digestion assay") measures the conversion of supercoiled double-stranded plasmid DNA to relaxed (nicked), linear, and degraded forms. The second assay ("linear DNA digestion assay") measured the conversion of linear double-stranded plasmid DNA to degraded forms. Specifically, DNase prepared according to the methods of the present invention is added to 160 microliters of a solution comprising 25 micrograms per milliliter of either supercoiled plasmid DNA or EcoRI-digested linearized plasmid DNA in 25 mM HEPES, pH 7.1, 100 µg/ml bovine serum albumin, 1 mM MgCl<sub>2</sub>, 2.5 mM CaCl<sub>2</sub>, 150 mM NaCl, and the samples are incubated at room temperature. At various times, aliquots of the reaction mixtures are removed and quenched by the addition of 25 mM EDTA, together with xylene cyanol, bromophenol blue, and glycerol. The integrity of the plasmid DNA in the quenched samples is analyzed by electrophoresis of the samples on agarose gels. After electrophoresis, the gels are stained with a solution of ethidium bromide and the DNA in the gels is visualized by ultraviolet light. The relative amounts of supercoiled, relaxed, and linear forms of plasmid DNA are determined by scanning the gels with a fluorescent imager (such as the Molecular Dynamics Model 575 FluorImager) and quantitating the amount of DNA in the bands of the gel that correspond to the different forms.

#### P. Insulin

The invention further includes a method for remodeling insulin. Insulin is well known as the most effective treatment for type I diabetes, in which the beta islet cells of the pancreas do not produce insulin for the regulation of blood glucose levels. The ramifications of diabetes and uncontrolled blood glucose include circulatory and foot problems, and blindness, not to mention a variety of other complications that either result from or are exacerbated by diabetes.

Prior to the cloning and sequencing of human insulin, porcine insulin was used as a treatment for diabetes. Insulin is now produced recombinantly, but the short, 51 amino acid sequence of the mature molecule is a complex structure comprising multiple sulfide bonds.

Current methods to recombinantly produce insulin result in a product that lacks similarity to

the native protein as produced in healthy non-diabetic subjects. The present invention seeks to repair this flaw.

A remodeled insulin peptide may be administered to a patient selected from the group consisting of a patient having Type I Diabetes (diabetes mellitus) and a patient having Type 2 diabetes mellitus who requires basal (long-acting) insulin for the control of hyperglycemia. A remodeled insulin peptide may also be administered to a diabetic patient to control hyperglycemia. Preferably, the patient is a human patient.

The nucleotide and amino acid sequence of human insulin is portrayed in SEQ ID NO:43 and SEQ ID NO:44, respectively (Figure 75A and 75B, respectively). Variants of insulin are abundant throughout the art. U.S. Patent No. 6,337,194 describes insulin fusion protein analogs, U.S. Patent No. 6,323,311 describes insulin derivatives comprising a cyclic anhydride of a dicarboxylic acid, and U.S. Patent No. 6,251,856 describes an insulin derivative comprising multiple amino acid substitutions and a lipophilic group. The skilled artisan will recognize that the following examples of insulin derivatives are in no way exhaustive, but simply represent a small sample of those well known in the art. Therefore, the present invention comprises insulin derivatives known or to be discovered.

Expression systems for the production of insulin are well known in the art, and can be accomplished using molecular biology techniques as described in, for example, Sambrook et al. (1989, Molecular Cloning: A Laboratory Manual, Cold Spring Harbor Laboratory Press, New York).

Assays to determine the functionality of an insulin molecule prepared according to the methods of the present invention are similarly well known in the art. For example, an *in vivo* model of glucose depression can be used to evaluate the biological activity of insulin synthesized using the methods of the present invention. Useful for this purpose is a rat model. The animals are fasted overnight (16 hours) prior to the experiment, and then anesthetized with intraperitoneally administered sodium pentobarbital or another suitable anesthetic such as ketamine. Each animal receives an i.v. injection (tail vein) of the particular insulin derivative (20 µg/ml/kg). Blood samples are taken from the jugular vein 15 and 5 minutes before injection and 15, 30, 60, 90, 120, 180, and 240 minutes after injection. Blood glucose levels are measured with a blood glucose monitor, available from a variety of commercial suppliers.

Q. Hepatitis B Vaccines (HBsAg)

The present invention further comprises a method for the remodeling the antigen used in hepatitis B vaccines (HbsAg or Hepatitis B sAg). HBsAg is a recombinantly produced surface antigen of the hepatitis B S-protein, and is used to illicit an immune response to the hepatitis B virus, an increasing dangerous virus that results in, among other things, liver disease including cirrhosis and carcinoma, and results in over 1 million deaths worldwide annually. Currently the HBsAg vaccine is administered three times over a six month interval to illicit a protective and neutralizing immune response.

HBsAg is currently produced in yeast strains, and therefore reflects the glycosylation patterns native to a fungus. The present invention provides a method to remodel HBsAg, resulting in among other things, improved immunogenicity, antibodies with improved affinity for the virus, and the like.

A remodeled HBsAg peptide may be administered to a patient to immunize the patient against disease caused by a Hepatitis B virus. A remodeled HBsAg peptide may also be administered to a predialysis patient or a dialysis patient to immunize the patient against disease caused by a Hepatitis B virus. Preferably, the patient is a human patient.

The sequences of the S-protein from a Hepatitis B virus (HBsAg) nucleic acid and primary amino acid chain are set forth herein as SEQ ID NO:45 and SEQ ID NO:46 (Figure 76A and 76B, respectively). The nucleotide is 1203 bases in length. The amino acid is 400 residues long. The last 226 amino acid residues are the small S-antigen, which is used in the GlaxoSmithKline vaccine and the Merck vaccine. Fifty-five amino acids upstream from the small S-antigen is the Pre-S start codon. The Pre-S + S regions are the middle S antigen, which is used in the Aventis Pasteur vaccine. From the first start codon to the Pre-S start codon comprises the rest of the S-protein, and is called the large S-protein. This is but one example of the HBsAg used in vaccines, and other subtypes are well known, as exemplified in GenBank Acc Nos.: AF415222, AF415221, AF415220, and AF415219. The sequences presented herein are simply examples of HBsAg known in the art. Similar antigens have been isolated from other strains of hepatitis B virus, and may or may not have been evaluated for antigenicity and potential as vaccine candidates. The present invention therefore encompasses hepatitis B vaccine S-protein surface antigens known or to be discovered.

Expression of an HBsAg in an expression system is a routine procedure for one of skill in the art, and is described in, for example, U.S. Patent No. 5,851,823. Assays for the immunogenicity of a vaccine are well known in the art, and comprise various tests for the production of neutralizing antibodies, and employ techniques such as ELISA, neutralization assays, Western blots, immunoprecipitation, and the like. Briefly, a sandwich ELISA for the detection of effective anti-HBsAg antibodies is described. The Enzygnost HBsAg assay (Aventis Behring, King of Prussia, PA) is used for such methods. Wells are coated with anti-HBs. Serum plasma or purified protein and appropriate controls are added to the wells and incubated. After washing, peroxidase-labeled antibodies to HBsAg are reacted with the remaining antigenic determinants. The unbound enzyme-linked antibodies are removed by washing and the enzyme activity on the solid phase is determined by methods well known in the art. The enzymatically catalyzed reaction of hydrogen peroxide and chromogen is stopped by adding diluted sulfuric acid. The color intensity is proportional to the HBsAg concentration of the sample and is obtained by photometric comparison of the color intensity of the unknown samples with the color intensities of the accompanying negative and positive control sera.

#### R. Human Growth Hormone

The present invention further encompasses a method for the remodeling of human growth hormone (HGH). The isoform of HGH which is secreted in the human pituitary, consists of 191 amino acids and has a molecular weight of about 21,500. The isoform of HGH which is made in the placenta is a glycosylated form. HGH participates in much of the regulation of normal human growth and development, including linear growth (somatogenesis), lactation, activation of macrophages, and insulin-like and diabetogenic effects, among others.

HGH is a complex hormone, and its effects are varied as a result of interactions with various cellular receptors. While compositions comprising HGH have been used in the clinical setting, especially to treat dwarfism, the efficacy is limited by the absence of glycosylation of the HGH produced recombinantly.

A remodeled HGH peptide may be administered to a patient selected from the group consisting of a patient having a growth hormone deficiency, a patient having Turner

syndrome, a patient having growth failure due to a lack of adequate endogenous growth hormone secretion, a patient having growth failure due to Prader-Willi syndrome (PWS), a patient having growth failure associated with chronic renal insufficiency, and a patient having AIDS associated wasting or cachexia. A remodeled HGH peptide may also be administered to a patient having short stature. Preferably, the patient is a human patient.

The nucleic and amino acid sequence of HGH are set forth elsewhere herein as SEQ ID NO:47 and SEQ ID NO:48 (Figure 77A and 77B, respectively). The skilled artisan will recognize that variants, derivatives, and mutants of HGH are well known. Examples can be found in U.S. Patent No. 6,143,523 where amino acid residues at positions 10, 14, 18, 21, 167, 171, 174, 176 and 179 are substituted, and in U.S. Patent No. 5,962,411 describes splice variants of HGH. The present invention encompasses these HGH variants known in the art of to be discovered.

Methods for the expression of HGH in recombinant cells is described in, for example, U.S. Patent No. 5,795,745. Methods for expression of HGH in, *inter alia*, prokaryotes, eukaryotes, insect cell systems, plants, and *in vitro* translation systems are well known in the art.

An HGH molecule produced using the methods of the current invention can be assayed for activity using a variety of methods known to the skilled artisan. For example, U.S. Patent 5,734,024 describes a method to determine the biological functionality of an expressed HGH.

### S. Anti-Thrombin III

Antithrombin (antithrombin III, AT-III) is a potent inhibitor of the coagulation cascade in blood. It is a non-vitamin K-dependent protease that inhibits the action of thrombin as well as other procoagulant factors (e.g., Factor Xa). Congenital antithrombin III deficiency is an autosomal dominant disorder in which an individual inherits one copy of a defective gene. This condition leads to increased risk of venous and arterial thrombosis, with onset of clinical manifestations typically presenting in young adulthood. Severe congenital antithrombin III deficiency, in which the individual inherits two defective genes, is an autosomal recessive condition associated with increased thrombogenesis, typically noted in infancy. Acquired antithrombin III deficiency most commonly is seen in situations where

there is inappropriate activation of the coagulation system. Common conditions that result in acquired antithrombin III deficiency include disseminated intravascular coagulation, microangiopathic hemolytic anemias due to endothelial damage (i.e., Hemolytic-uremic syndrome), and veno-occlusive disease (VOD) seen in patients undergoing bone marrow transplant. AT-III deficiency may be corrected acutely by infusions of AT-III concentrates.

A remodeled AT-III peptide may be administered to a patient selected from the group consisting of a patient having a hereditary AT-III deficiency in connection with a surgical or obstetrical procedure and a hereditary AT-III deficient patient having a thromboembolism. Preferably, the patient is a human patient.

Antithrombin III (AT-III) is an  $\alpha_2$ -glycoprotein of molecular weight 58,000. It is sold commercially as Thrombate III™ (Bayer Corp., West Haven, CT). The nucleic acid and amino acid sequences of human antithrombin III are displayed in Figure 78A (SEQ ID NO:63) and 78B (SEQ ID NO:64), respectively.

Methods to make anti-thrombin III are well known to those in the art. For example, published nucleic acid and amino acid sequences are available for human antithrombin III (see, U.S. Patent No. 4,517,294) and mutants of human antithrombin III (see, U.S. Patent Nos. 5,420,252, 5,618,713, 5,700,663). The methods of the invention may be used with any of these amino acid sequences and any nucleic acid sequences that encode them, but are not limited to these sequences. Exemplary methods to produce recombinant antithrombin III are well known in the art, and several are described in U.S. Patent Nos. 5,420,252, 5,843,705, 6,441,145 and 5,994,628. Exemplary methods to purify recombinant antithrombin III are described in U.S. Patent Nos. 5,989,593, 6,268,487, 6,395,888, 6,395,881, 6,451,978 and 6,518,406.

There are many known uses for recombinant antithrombin III. Antithrombin III can be used as an anticoagulant during surgery (U.S. Patent Nos. 5,252,557, 5,182,259), as part of a pharmaceutical preparation or method to inhibit thrombosis (U.S. Patent Nos. 5,565,471, 6,001,820), and to reduce the adverse side effects of cellular transplantation (U.S. Patent No. 6,387,366). Additionally, antithrombin III preparations can be used to increase placental blood flow (U.S. Patent No. 5,888,964), inhibit fertilization (U.S. Patent No. 5,545,615), treat asthma (U.S. Patent No. 6,355,626) and treat arthritis (U.S. Patent No. 5,252,557) and other inflammatory processes (U.S. Patent No. 6,399,572). Antithrombin III can also be used to

manufacture replacement blood plasma (U.S. Patent Nos. 4,900,720) or prepare a stabilized cellular blood product (U.S. Patent No. 6,139,878) for transfusions. Antithrombin III may be administered as a pharmaceutical preparation (U.S. Patent Nos. 5,084,273, 5,866,122, 6,399,572, 6,156,731 and 6,514,940) or using gene therapy methodology (U.S. Patent No. 6,410,015). Compositions comprising antithrombin III can be used as tissue adhesives (U.S. Patent No. 6,500,427) or lubricants for medical devices that are introduced to the patient (U.S. Patent No. 6,391,832). Antithrombin III can also be used to coat endovascular stents (U.S. Patent Nos. 6,355,055, 6,240,616, 5,985,307, 5,685,847 and 5,222,971), ocular implants (U.S. Patent No. 5,944,753) and prostheses in general (U.S. Patent Nos. 6,503,556, 6,491,965 and 6,451,373). Antithrombin III can also be used in methods to locate an internal bleeding site in a patient (U.S. Patent No. 6,314,314) and to determine hemostatic dysfunction in a patient (U.S. Patent No. 6,429,017).

#### T. Human Chorionic Gonadotropin

Human Chorionic Gonadotropin (hCG) is a glycoprotein composed of an alpha subunit and a beta subunit. HCG is closely related to two other gonadotropins, luteinizing hormone (LH) and follicle stimulating hormone (FSH), as well as thyroid stimulating hormone (TSH), all three of which are glycoprotein hormones. The alpha subunits of these various glycoprotein hormones are structurally very similar, but the beta subunits differ in amino acid sequence.

The nucleic acid and amino acid sequences of the human chorionic gonadotropin  $\alpha$ -subunit are displayed in Figures 79A (SEQ ID NO:69) and 79B (SEQ ID NO:70), respectively. The nucleic acid and amino acid sequences of the human chorionic gonadotropin  $\beta$ -subunit are displayed in Figures 79C (SEQ ID NO:71) and 79D (SEQ ID NO:72), respectively.

Human chorionic gonadotropin is used in an infertility treatment to promote ovulation or release of an egg from the ovary in women who do not ovulate on their own. Human chorionic gonadotropin is also given to young males to treat undescended or underdeveloped testicles. It is used in men to stimulate the production of testosterone. Some physicians also prescribe human chorionic gonadotropin for men having erectile dysfunction or lack of sexual desire, and for treatment of male "menopause."

A remodeled hCG peptide may be administered to a patient selected from the group consisting of a patient undergoing assisted reproductive technology (ART), a patient undergoing *in vitro* fertilization (IVF), a patient undergoing embryo transfer, an infertile patient, a male patient having prepubertal cryptorchidism not due to anatomical obstruction, and a male patient having hypogonadotropic hypogonadism. A remodeled hCG peptide may also be administered to induce final follicular maturation and early luteinization in an infertile female patient, wherein the infertile female patient has undergone pituitary desensitization and pretreatment with follicle stimulating hormones. A remodeled hCG peptide may also be administered to induce ovulation and pregnancy in an anovulatory infertile patient.

Preferably, the patient is a human patient.

Methods to make human chorionic gonadotropin are well known in the art. The heterodimeric hCG can be recombinantly made in any one of many expression systems currently used for industrial manufacture of recombinant proteins. One method of making recombinant hCG is described in U.S. Patent No. 5,639,639. Methods for making recombinant heterodimeric proteins by expressing both subunits in the same cell are, in general, well known in the art, and several methods are described in the U.S. Patent Nos. 5,643,745 (expression in a filamentous fungus), 5,985,611 and 6,087,129 (expression in secretory cells). Alternatively, each subunit can be expressed individually in cells, and the two subunits later brought together *in vitro* for assembly into the heterodimer.

Methods for using human chorionic gonadotropin are numerous and well known in the art. Commonly, hCG is used to induce or synchronize ovulation in mammals (see, U.S. Patent Nos. 6,489,288, 5,589,457, 5,532,155, 4,196,123, 4,062,942 and 4,845,077). Additionally, hCG can be used in pregnancy tests, and in particular agglutination-based tests (see, U.S. Patent Nos. 3,991,175, 4,003,988, 4,071,314 and 4,088,749). hCG can also be used in a contraceptive vaccine (see, U.S. Patent Nos. 4,161,519 and 4,966,888). In addition, hCG can be used to treat conditions related to aging and altered hormonal balance such as benign prostatic hypertrophy (see, U.S. Patent No. 5,610,136) and central nervous system diseases common in the elderly (see, U.S. Patent No. 4,791,099).

Alternatively, hCG can be used to detect and treat cancers that express hCG or one of its subunits. hCG-expressing tumors include, but are not limited to, breast, prostate, ovary and stomach carcinomas, and neuroblastomas such as Kaposi's sarcoma. Antibodies can be

raised to hCG which has been glycoremodeled so as to have glycan structures similar to those found on the tumor-expressed hCG, and these antibodies may be used to detect hCG-expressing tumors in patients according to methods well known in the art (see, U.S. Patent Nos. 4,311,688, 4,478,815 and 4,323,546). Additionally, remodeled hCG can be used to

5 raise an immune response to a tumor that is expressing hCG (see, U.S. Patent Nos. 5,677,275, 5,762,931, 5,877,148, 4,970,071 and 4,966,753).

hCG can also be used in methods to generally immunomodulate an animal, such as described in U.S. Patent Nos. 5,554,595, 5,851,997 and 5,700,781. In addition, hCG can be used as an inhibitor of the matrix metalloprotease in conditions benefiting from such

10 treatment, such as chronic inflammatory diseases, multiple sclerosis and angiogenesis-dependent diseases (see, U.S. Patent No. 6,444,639).

#### U. $\alpha$ -Iduronidase

$\alpha$ -Iduronidase is sold commercially as Aldurazyme™ (BioMarin and Genzyme). It is

15 useful for replacement therapy for the treatment of MPS I, a lysosomal storage disease. MPS I (also known as Hurler disease) is a genetic disease caused by the deficiency of alpha-L-iduronidase, an enzyme normally required for the breakdown of certain complex carbohydrates known as glycosaminoglycans (GAGs). The normal breakdown of GAGs is incomplete or blocked if the enzyme is not present in sufficient quantity. The cell is then

20 unable to excrete the carbohydrate residues and they accumulate in the lysosomes of the cell and cause MPS I.

A remodeled alpha-iduronidase peptide may be administered to a patient selected from the group consisting of a patient having a lysosomal storage disease, a patient having an alpha-L-iduronidase deficiency, a patient having mucopolysaccharidosis I (MPS I), and a

25 patient having Hurler disease. Preferably, the patient is a human patient.

Methods to produce and purify  $\alpha$ -iduronidase, as well as methods to treat certain genetic disorders including  $\alpha$ -L-iduronidase deficiency and mucopolysaccharidosis I (MPS 1) are described in U.S. Patent No. 6,426,208. The nucleic acid and amino acid sequences of human  $\alpha$ -iduronidase are found in Figures 80A (SEQ ID NO:65) and 80B (SEQ ID NO:66),  
5 respectively.

#### V. $\alpha$ -Galactosidase A

$\alpha$ -Galactosidase A (also known as agalsidase beta) is sold commercially as Fabrazyme™ (Genzyme).  $\alpha$ -Galactosidase A is useful for the treatment of Fabry disease.

10 Fabry disease is a rare, inherited disorder caused by the deficiency of the essential enzyme  $\alpha$ -galactosidase. Without this enzyme, Fabry patients are unable to breakdown a fatty acid substance in their body called globotriaosylceramide (GL-3), which accumulates in cells in the blood vessels of the heart, kidney, brain and other vital organs. The progressive buildup of this substance puts patients a risk for stroke, heart attack, kidney damage and debilitating  
15 pain. Most patients develop kidney failure during adulthood, and severe organ complications lead to death around age forty.

A remodeled alpha-galactosidase A peptide may be administered to a patient selected from the group consisting of a patient having a lysosomal storage disease, a patient having an alpha-galactosidase A deficiency, and a patient having Fabry disease. Preferably, the patient  
20 is a human patient.

The  $\alpha$ -galactosidase A enzyme is a lysosomal enzyme which hydrolyzes globotriaosylceramide and related glycolipids which have terminal  $\alpha$ -galactosidase linkages. It is a 45 kDa N-glycosylated protein encoded on the long arm of the X chromosome. The initial glycosylated forms (Mr=55,000 to 58,000) synthesized in human fibroblasts or Chang  
25 liver cells are processed to a mature glycosylated form (Mr=50,000). The mature active enzyme as purified from human tissues and plasma is a homodimer (Bishop et al., 1986, Proc. Natl. Acad. Sci. USA 83: 4859-4863). The nucleic acid and amino acid sequences of  $\alpha$ -galactosidase A are found in Figures 81A (SEQ ID NO:67) and 81B (SEQ ID NO:68). Other useful nucleic acid and amino acid sequences of alpha-galactosidase A are found in  
30 U.S. Patent No. 6,329,191.

References teaching how to make alpha-galactosidase A are found in U.S. Patent Nos. 5,179,023 and 5,658,567 (expression in insect cells), U.S. Patent No. 5,356,804 (expression and secretion from mammalian cells, including CHO cells), U.S. Patent No. 5,401,451 (expression in mammalian cells), U.S. Patent No. 5,580,757 (expression in mammalian cells as a fusion protein) and U.S. Patent No. 5,929,304 (expression in plant cells). Methods for purifying recombinant alpha-galactosidase A are found in U.S. Patent No. 6,395,884.

References teaching how to use alpha-galactosidase A to treat patients include, but are not limited to, U.S. Patent No. 6,066,626 (gene therapy) and U.S. Patent No. 6,461,609 (treatment with the protein). Mutant forms of alpha-galactosidase A that are useful in the methods of the invention include, but are not limited to, those described in U.S. Patent No. 6,210,666.

#### W. Antibodies

The present invention further comprises a method for the remodeling of various antibody preparations including chimeric antibody preparations, including, chimeric TNFR, chimeric anti-glycoprotein IIb/IIIa, chimeric anti-HER2, chimeric anti-RSV, chimeric anti-CD20, and chimeric anti-TNF. Chimeric antibody preparations comprise a human Fc portion from an IgG antibody and the variable regions from a monoclonal antibody specific for an antigen. Other preparations comprise a receptor, for example the 75 kDa TNF receptor, fused to a human IgG Fc portion. These molecules further include Fab fragments comprising light and heavy chains from human and mice. A chimeric TNFR is useful in the treatment of inflammatory diseases, such as rheumatoid arthritis. Chimeric anti-glycoprotein IIb/IIIa is useful in the treatment of cardiac abnormalities, blood clotting, and platelet function disturbances. A chimeric anti-HER2 is useful as a treatment for breast cancer, chimeric anti-RSV is useful for the treatment of respiratory syncytial virus, chimeric anti-CD20 is useful for the treatment of Non-Hodgkin's lymphoma, and chimeric anti-TNF is used for treatment of Crohn's disease.

While these chimeric antibodies have proved useful in the management of varied diseases, administration has to be fairly frequent and at fairly high doses due to the relatively short half-life of a recombinant protein produced in rodent cells. While a majority of the chimeric antibody is human, and therefore regarded as "self" by the immune system, they are

degraded and destroyed due to non-native glycosylation patterns. The present invention proposes to repair this problem, greatly increasing the efficacy of these novel medicines.

#### Antibodies and Methods of their Generation

The term "antibody," as used herein, refers to an immunoglobulin molecule which is  
5 able to specifically bind to a specific epitope on an antigen. Antibodies can be intact immunoglobulins derived from natural sources or from recombinant sources and can be immunoreactive portions of intact immunoglobulins. Antibodies are typically tetramers of immunoglobulin molecules. The antibodies in the present invention may exist in a variety of forms including, for example, polyclonal antibodies, monoclonal antibodies, Fv, Fab and  
10 F(ab)<sub>2</sub>, as well as single chain antibodies and humanized antibodies (Harlow et al., 1999, Using Antibodies: A Laboratory Manual, Cold Spring Harbor Laboratory Press, NY; Harlow et al., 1989, Antibodies: A Laboratory Manual, Cold Spring Harbor, New York; Houston et al., 1988, Proc. Natl. Acad. Sci. USA 85:5879-5883; Bird et al., 1988, Science 242:423-426).

By the term "synthetic antibody" as used herein, is meant an antibody which is  
15 generated using recombinant DNA technology, such as, for example, an antibody expressed by a bacteriophage as described herein. The term should also be construed to mean an antibody which has been generated by the synthesis of a DNA molecule encoding the antibody and which DNA molecule expresses an antibody peptide, or an amino acid sequence specifying the antibody, wherein the DNA or amino acid sequence has been obtained using  
20 synthetic DNA or amino acid sequence technology which is available and well known in the art.

Monoclonal antibodies directed against full length or peptide fragments of a peptide or peptide may be prepared using any well known monoclonal antibody preparation procedures, such as those described, for example, in Harlow et al. (1988, In: Antibodies, A  
25 Laboratory Manual, Cold Spring Harbor, NY) and in Tuszynski et al. (1988, Blood, 72:109-115). Quantities of the desired peptide may also be synthesized using chemical synthesis technology. Alternatively, DNA encoding the desired peptide may be cloned and expressed from an appropriate promoter sequence in cells suitable for the generation of large quantities of peptide. Monoclonal antibodies directed against the peptide are generated from mice  
30 immunized with the peptide using standard procedures as referenced herein.

Nucleic acid encoding the monoclonal antibody obtained using the procedures described herein may be cloned and sequenced using technology which is available in the art, and is described, for example, in Wright et al. (1992, Critical Rev. in Immunol. 12(3,4):125-168) and the references cited therein. Further, the antibody of the invention may be

5 "humanized" using the technology described in Wright et al., (*supra*) and in the references cited therein, and in Gu et al. (1997, Thrombosis and Hematocyst 77(4):755-759).

To generate a phage antibody library, a cDNA library is first obtained from mRNA which is isolated from cells, e.g., the hybridoma, which express the desired peptide to be expressed on the phage surface, e.g., the desired antibody. cDNA copies of the mRNA are  
10 produced using reverse transcriptase. cDNA which specifies immunoglobulin fragments are obtained by PCR and the resulting DNA is cloned into a suitable bacteriophage vector to generate a bacteriophage DNA library comprising DNA specifying immunoglobulin genes. The procedures for making a bacteriophage library comprising heterologous DNA are well known in the art and are described, for example, in Sambrook and Russell (2001, Molecular  
15 Cloning: A Laboratory Manual, Cold Spring Harbor, NY).

Bacteriophage which encode the desired antibody, may be engineered such that the peptide is displayed on the surface thereof in such a manner that it is available for binding to its corresponding binding peptide, e.g., the antigen against which the antibody is directed. Thus, when bacteriophage which express a specific antibody are incubated in the presence of  
20 a cell which expresses the corresponding antigen, the bacteriophage will bind to the cell. Bacteriophage which do not express the antibody will not bind to the cell. Such panning techniques are well known in the art and are described for example, in Wright et al., (*supra*).

Processes such as those described above, have been developed for the production of human antibodies using M13 bacteriophage display (Burton et al., 1994, Adv. Immunol.  
25 57:191-280). Essentially, a cDNA library is generated from mRNA obtained from a population of antibody-producing cells. The mRNA encodes rearranged immunoglobulin genes and thus, the cDNA encodes the same. Amplified cDNA is cloned into M13 expression vectors creating a library of phage which express human antibody fragments on their surface. Phage which display the antibody of interest are selected by antigen binding  
30 and are propagated in bacteria to produce soluble human immunoglobulin. Thus, in contrast

to conventional monoclonal antibody synthesis, this procedure immortalizes DNA encoding human immunoglobulin rather than cells which express human immunoglobulin.

Remodeling glycans of antibody molecules

5 The specific glycosylation of one class of peptides, namely immunoglobulins, has a particularly important effect on the biological activity of these peptides. The invention should not be construed to be limited solely to immunoglobulins of the IgG class, but should also be construed to include immunoglobulins of the IgA, IgE and IgM classes of antibodies.

10 Further, the invention should not be construed to be limited solely to any type of traditional antibody structure. Rather, the invention should be construed to include all types of antibody molecules, including, for example, fragments of antibodies, chimeric antibodies, human antibodies, humanized antibodies, etc.

15 A typical immunoglobulin molecule comprises an effector portion and an antigen binding portion. For a review of immunoglobulins, see Harlow et al., 1988, Antibodies: A Laboratory Manual, Cold Spring Harbor, New York, and Harlow et al., 1999, Using Antibodies: A Laboratory Manual, Cold Spring Harbor Laboratory Press, NY. The effector portion of the immunoglobulin molecule resides in the Fc portion of the molecule and is responsible in part for efficient binding of the immunoglobulin to its cognate cellular receptor. Improper glycosylation of immunoglobulin molecules particularly in the CH2 domain of the Fc portion of the molecule, affects the biological activity of the  
20 immunoglobulin.

More specifically with respect to the immunoglobulin IgG, IgG effector function is governed in large part by whether or not the IgG contains an N-acetylglucosamine (GlcNAc) residue attached at the 4-O position of the branched mannose of the trimannosyl core of the N-glycan at Asparagine (Asn) 297 in the CH2 domain of the IgG molecule. This residue is  
25 known as a "bisecting GlcNAc." The purpose of adding bisecting GlcNAc to the N-glycan chains of a natural or recombinant IgG molecule or a IgG-Fc-containing chimeric construct is to optimize Fc immune effector function of the Fc portion of the molecule. Such effector functions may include antibody-dependent cellular cytotoxicity (ADCC) and any other biological effects that require efficient binding to FcγR receptors, and binding to the C1  
30 component of complement. The importance of bisecting GlcNAc for achieving maximum

immune effector function of IgG molecules has been described (Lifely et al., 1995, Glycobiology 5 (8): 813-822; Jeffris et al., 1990, Biochem. J. 268 (3): 529-537).

The glycans found at the N-glycosylation site at Asn 297 in the CH2 domain of IgG molecules have been structurally characterized for IgG molecules found circulating in human and animal blood plasma, IgG produced by myeloma cells, hybridoma cells, and a variety of transfected immortalized mammalian and insect cell lines. In all cases the N-glycan is either a high mannose chain or a complete (Man3, GlcNAc4, Gal2, NeuAc2, Fuc1) or variably incomplete biantennary chain with or without bisecting GlcNAc (Raju et al., 2000, Glycobiology 10 (5): 477-486; Jeffris et al., 1998, Immunological. Rev. 163L59-76; Lerouge et al., 1998, Plant Mol. Biol. 38: 31-48; James et al., 1995, Biotechnology 13: 592-596).

The present invention provides an *in vitro* customized glycosylated immunoglobulin molecule. The immunoglobulin molecule may be any immunoglobulin molecule, including, but not limited to, a monoclonal antibody, a synthetic antibody, a chimeric antibody, a humanized antibody, and the like. Specific methods of generating antibody molecules and their characterization are disclosed elsewhere herein. Preferably, the immunoglobulin is IgG, and more preferably, the IgG is a humanized or human IgG, most preferably, IgG1.

The present invention specifically contemplates using  $\beta$ 1,4-mannosyl-glycopeptide  $\beta$ 1,4-N-acetylglucosaminyltransferase, GnT-III: EC2.4.1.144 as an *in vitro* reagent to glycosidically link N-acetylglucosamine (GlcNAc) onto the 4-O position of the branched mannose of the trimannosyl core of the N-glycan at Asn 297 in the CH2 domain of an IgG molecule. However, as will be appreciated from the disclosure provided herein, the invention should not be construed to solely include the use of this enzyme to provide a bisecting GlcNAc to an immunoglobulin molecule. Rather, it has been discovered that it is possible to modulate the glycosylation pattern of an antibody molecule such that the antibody molecule has enhanced biological activity, i.e., effector function, in addition to potential enhancement of other properties, e.g., stability, and the like.

There is provided in the present invention a general method for removing fucose molecules from the Asn(297) N-linked glycan for the purpose of enhancing binding to Fc-gammaRIIIA, and enhanced antibody-dependent cellular cytotoxicity (see, Shields et al., 2002, J. Biol. Chem. 277:26733-26740). The method entails contacting the antibody molecule with a fucosidase appropriate for the linkage of the fucose molecule(s) on the

antibody glycan(s). Alternately, the recombinant antibody can be expressed in cells that do express fucosyltransferases, such as the Lec13 variant of CHO cells. The removal of fucose from the glycan(s) of the antibody can be done alone, or in conjunction with other methods to remodel the glycans, such as adding a bisecting GlcNAc. Expression of antibodies in cells lacking GnT-I may also result in Fc glycans lacking core fucose, which can be further modified by the present invention.

There is provided in the present invention a general method for introducing a bisecting GlcNAc for the purpose of enhancing Fc immune effector function in any preparation of IgG molecules containing N-linked oligosaccharides in the CH2 domain, typically at Asn 297. The method requires that the population of IgG molecules is brought to a state of glycosylation such that the glycan chain is an acceptor for GnT-III. This is accomplished in any one of three ways: 1) by selection or genetic manipulation of a host expression system that secretes IgG with N-glycan chains that are substrates for GnT-III; 2) by treatment of a population of IgG glycoforms with exoglycosidases such that the glycan structure(s) remaining after exoglycosidase treatment is an acceptor for GnT-III; 3) some combination of host selection and exoglycosidase treatment as in 1) and 2) above plus successive additions of GlcNAc by GnT-I and GnT-II to create an acceptor for GnT-III.

For example, IgG obtained from chicken plasma contains primarily high mannose chains and would require digestion with one or more  $\alpha$ -mannosidases to create a substrate for addition of GlcNAc to the  $\alpha$ 1,3 mannose branch of the trimannosyl core by GnT-I. This substrate could be the elemental trimannosyl core, Man3GlcNAc2. Treatment of this core structure with a combination of GnT-I, GnT-II, and GnT-III using UDP-GlcNAc as a sugar donor creates Man3GlcNAc5 as shown in Figure 1. The order of action of these glycosyltransferases may be varied to optimize the production of the desired product.

Optionally, this structure can then be extended by treatment with  $\beta$ 1,4 galactosyltransferase. If required, the galactosylated oligosaccharide can be further extended using  $\alpha$ 2,3- or  $\alpha$ 2,6-sialyltransferase to achieve a completed biantennary structure. Using this method biantennary glycan chains can be remodeled as required for the optimal Fc immune effector function of any therapeutic IgG under development (Figure 3).

Alternatively, IgG molecules found in the plasma of most animals or IgG which is secreted as a recombinant product by most animal cells or by transgenic animals typically

include a spectrum of biantennary glycoforms including complete (NeuAc2, Gal2, GlcNAc4, Man3,  $\pm$ Fuc1) (Figure 3) and variably incomplete forms, with or without bisecting GlcNAc (Raju et al., 2000, *Glycobiology* 10 (5): 477-486; Jeffris et al., 1998, *Immunological Rev.* 163: 59-76). To ensure that bisecting GlcNAc is present in the entire population of immunoglobulin molecules so produced, the mixture of molecules can be treated with the following exoglycosidases, successively or in a mixture: neuraminidase,  $\beta$ -galactosidase,  $\beta$ -hexosaminidase,  $\alpha$ -fucosidase. The resulting trimannosyl core can then be remodeled using glycosyltransferases as noted above.

In some cases it may be desired to abolish effector function from existing antibody molecules. The present invention also includes modifying the Fc glycans with appropriate glycosidases and glycosyltransferases to eliminate effector function. Also anticipated is the addition of sugars modified with PEG or other polymers that serve to hinder or abolish binding of Fc receptors or complement to the antibody.

In addition, IgG secreted by transgenic animals or stored as "plantibodies" by transgenic plants have been characterized. An IgG molecule produced in a transgenic plant having N-glycans that contain  $\beta$ 1,2 linked xylose and/or  $\alpha$ 1,3 linked fucose can be treated with exoglycosidases to remove those residues, in addition to the above described exoglycosidases in order to create the trimannosyl core or a Man3GlcNAc4 structure, and are then treated with glycosyltransferases to remodel the N-glycan as described above.

The primary novel aspect of the current invention is the application of appropriate glycosyltransferases, with or without prior exoglycosidase treatment, applied in the correct sequence to optimize the effector function of the antibody. In one exemplary embodiment, a bisecting GlcNAc is introduced into the glycans of IgG molecules or other IgG-Fc-chimeric constructs where bisecting GlcNAc is required. In another exemplary embodiment, the core fucose is removed from the glycans of IgG molecules or other IgG-Fc-chimeric constructs.

#### X. TNF receptor-IgG Fc fusion protein

The nucleotide and amino acid sequences of the 75 kDa human TNF receptor are set forth herein as SEQ ID NO:31 and SEQ ID NO:32, respectively (Figure 82A and 82B, respectively). The amino acid sequences of the light and heavy variable regions of chimeric anti-HER2 are set forth as SEQ ID NO:35 and SEQ ID NO:36, respectively (Figure 83A and

83B, respectively). The amino acid sequences of the heavy and light variable regions of chimeric anti-RSV are set forth as SEQ ID NO:38 and SEQ ID NO:37, respectively (Figure 84A and 84B, respectively). The amino acid sequences of the non-human variable regions of anti-TNF are set forth herein as SEQ ID NO:41 and SEQ ID NO:42, respectively (Figure 85A and 85B, respectively). The nucleotide and amino acid sequence of the Fc portion of human IgG is set forth as SEQ ID NO:49 and SEQ ID NO:50 (Figure 86A and 86B, respectively).

A remodeled chimeric ENBREL™ may be administered to a patient selected from the group consisting of a patient having rheumatoid arthritis and a patient having polyarticular-course juvenile arthritis. A remodeled chimeric ENBREL™ may also be administered to an arthritis patient to reduce signs, symptoms, or structural damage in the patient. Preferably, the patient is a human patient.

A remodeled Synagis™ antibody may be administered to a patient to immunize the patient against infection by respiratory syncytial virus (RSV). A remodeled Synagis™ antibody may also be administered to a patient to prevent or reduce the severity of a lower respiratory tract disease caused by RSV. Preferably, the patient is a human patient.

#### Y. MAb anti-glycoprotein IIb/IIIa

The amino acid sequences of a murine anti-glycoprotein IIb/IIIa antibody variable regions are set forth in SEQ ID NO:52 (murine mature variable light chain, Figure 87) and SEQ ID NO: 54 (murine mature variable heavy chain, Figure 88). These murine sequences can be combined with human IgG amino acid sequences SEQ ID NO:51 (human mature variable light chain, Figure 89), SEQ ID NO: 53 (human mature variable heavy chain, Figure 90), SEQ ID NO: 55 (human light chain, Figure 91) and SEQ ID NO: 56 (human heavy chain, Figure 92) according to the procedures found in U.S. Patent No. 5,777,085 to create a chimeric humanized murine anti-glycoprotein IIb/IIIa antibody. Other anti-glycoprotein IIb/IIIa humanized antibodies are found in U.S. Patent No. 5,877,006. A cell line expressing the anti-glycoprotein IIb/IIIa MAb 7E3 can be commercially obtained from the ATCC (Manassas, VA) as accession no. HB-8832.

#### Indications for selected antibodies

A remodeled Reopro™ may be administered to a patient selected from the group consisting of a patient undergoing percutaneous coronary intervention and a patient having unstable angina, wherein the patient is scheduled for percutaneous coronary intervention within 24 hours. A remodeled Reopro™ may also be administered to a patient undergoing  
5 percutaneous coronary intervention to reduce or prevent a cardiac ischemic complication in the patient. Preferably, the patient is a human patient.

A remodeled Herceptin™ may be administered to a patient having metastatic breast cancer that overexpresses the HER2 protein. Preferably, the patient is a human patient.

A remodeled Remicade™ antibody may be administered to a patient selected from the  
10 group consisting of a patient having rheumatoid arthritis, a patient having Crohn's disease, and a patient having fistulizing Crohn's disease. A remodeled Remicade™ antibody may also be administered to a rheumatoid arthritis patient to reduce signs and symptoms of rheumatoid arthritis in the patient. A remodeled Remicade™ antibody may also be administered to a Crohn's disease patient to reduce signs and symptoms of Crohn's disease in  
15 the patient. Preferably, the patient is a human patient.

#### Z. MAb anti-CD20

The nucleic acid and amino acid sequences of a chimeric anti-CD20 antibody are set forth in SEQ ID NO: 59 (nucleic acid sequence of murine variable region light chain, Figure  
20 93A), SEQ ID NO:60 (amino acid sequence of murine variable region light chain, Figure 93B), SEQ ID NO:61 (nucleic acid sequence of murine variable region heavy chain, Figure 94A) and SEQ ID NO:62 (amino acid sequence of murine variable region heavy chain, Figure 94B). In order to humanize a murine antibody, the TCAE 8 (SEQ ID NO:57, Figure 95A – 95E), which contains the human IgG heavy and light constant domains, may be  
25 conveniently used. By cloning the above murine variable region encoding DNA into the TCAE 8 vector according to instructions given in U.S. Patent No. 5,736,137, a vector is created (SEQ ID NO: 58, Figure 96A – 96E) which when transformed into a mammalian cell line, expresses a chimeric anti-CD20 antibody. Other humanized anti-CD20 antibodies are found in U.S. Patent No. 6,120,767. A cell line expressing the anti-CD20 MAb C273 can be  
30 commercially obtained from the ATCC (Manassas, VA) as accession no. HB-9303.

The skilled artisan will readily appreciate that the sequences set forth herein are not exhaustive, but are rather examples of the variable regions, receptors, and other binding moieties of chimeric antibodies. Further, methods to construct chimeric or "humanized" antibodies are well known in the art, and are described in, for example, U.S. Patent No. 6,329,511 and U.S. Patent No. 6,210,671. Coupled with the present disclosure and methods well known throughout the art, the skilled artisan will recognize that the present invention is not limited to the sequences disclosed herein.

The expression of a chimeric antibody is well known in the art, and is described in detail in, for example, U.S. Patent No. 6,329,511. Expression systems can be prokaryotic, eukaryotic, and the like. Further, the expression of chimeric antibodies in insect cells using a baculovirus expression system is described in Putlitz et al. (1990, Bio/Technology 8:651-654). Additionally, methods of expressing a nucleic acid encoding a fusion or chimeric protein are well known in the art, and are described in, for example, Sambrook et al. (2001, Molecular Cloning: A Laboratory Manual, Cold Spring Harbor Laboratory Press, New York) and Ausubel et al. (1997, Current Protocols in Molecular Biology, Green & Wiley, New York).

Determining the function and biological activity of a chimeric antibody produced according to the methods of the present invention is a similarly basic operation for one of skill in the art. Methods for determining the affinity of an antibody by competition assays are detailed in Berzofsky (J. A. Berzofsky and I. J. Berkower, 1984, in Fundamental Immunology (ed. W. E. Paul), Raven Press (New York), 595). Briefly, the affinity of the chimeric antibody is compared to that of the monoclonal antibody from which it was derived using a radio-iodinated monoclonal antibody.

A remodeled anti-CD20 antibody may be administered to a patient having relapsed or refractory low grade or follicular, CD20-positive, B-cell non-Hodgkin's lymphoma. Preferably, the patient is a human patient.

#### VII. Pharmaceutical Compositions

In another aspect, the invention provides a pharmaceutical composition. The pharmaceutical composition includes a pharmaceutically acceptable diluent and a covalent conjugate between a non-naturally-occurring, water-soluble polymer, therapeutic moiety or biomolecule and a glycosylated or non-glycosylated peptide. The polymer, therapeutic

moiety or biomolecule is conjugated to the peptide via an intact glycosyl linking group interposed between and covalently linked to both the peptide and the polymer, therapeutic moiety or biomolecule.

Pharmaceutical compositions of the invention are suitable for use in a variety of drug delivery systems. Suitable formulations for use in the present invention are found in  
5 *Remington's Pharmaceutical Sciences*, Mace Publishing Company, Philadelphia, PA, 17th ed. (1985). For a brief review of methods for drug delivery, see, Langer, *Science* **249**:1527-1533 (1990).

The pharmaceutical compositions may be formulated for any appropriate manner of administration, including for example, topical, oral, nasal, intravenous, intracranial,  
10 intraperitoneal, subcutaneous or intramuscular administration. For parenteral administration, such as subcutaneous injection, the carrier preferably comprises water, saline, alcohol, a fat, a wax or a buffer. For oral administration, any of the above carriers or a solid carrier, such as mannitol, lactose, starch, magnesium stearate, sodium saccharine, talcum, cellulose, glucose,  
15 sucrose, and magnesium carbonate, may be employed. Biodegradable microspheres (*e.g.*, polylactate polyglycolate) may also be employed as carriers for the pharmaceutical compositions of this invention. Suitable biodegradable microspheres are disclosed, for example, in U.S. Patent Nos. 4,897,268 and 5,075,109.

Commonly, the pharmaceutical compositions are administered parenterally, *e.g.*,  
20 intravenously. Thus, the invention provides compositions for parenteral administration which comprise the compound dissolved or suspended in an acceptable carrier, preferably an aqueous carrier, *e.g.*, water, buffered water, saline, PBS and the like. The compositions may contain pharmaceutically acceptable auxiliary substances as required to approximate physiological conditions, such as pH adjusting and buffering agents, tonicity adjusting agents,  
25 wetting agents, detergents and the like.

These compositions may be sterilized by conventional sterilization techniques, or may be sterile filtered. The resulting aqueous solutions may be packaged for use as is, or lyophilized, the lyophilized preparation being combined with a sterile aqueous carrier prior to administration. The pH of the preparations typically will be between 3 and 11, more  
30 preferably from 5 to 9 and most preferably from 7 and 8.

In some embodiments the peptides of the invention can be incorporated into liposomes formed from standard vesicle-forming lipids. A variety of methods are available for preparing liposomes, as described in, *e.g.*, Szoka *et al.*, *Ann. Rev. Biophys. Bioeng.* **9**: 467 (1980), U.S. Pat. Nos. 4,235,871, 4,501,728 and 4,837,028. The targeting of liposomes using  
5 a variety of targeting agents (*e.g.*, the sialyl galactosides of the invention) is well known in the art (*see, e.g.*, U.S. Patent Nos. 4,957,773 and 4,603,044).

Standard methods for coupling targeting agents to liposomes can be used. These methods generally involve incorporation into liposomes of lipid components, such as phosphatidylethanolamine, which can be activated for attachment of targeting agents, or  
10 derivatized lipophilic compounds, such as lipid-derivatized peptides of the invention.

Targeting mechanisms generally require that the targeting agents be positioned on the surface of the liposome in such a manner that the target moieties are available for interaction with the target, for example, a cell surface receptor. The carbohydrates of the invention may be attached to a lipid molecule before the liposome is formed using methods known to those  
15 of skill in the art (*e.g.*, alkylation or acylation of a hydroxyl group present on the carbohydrate with a long chain alkyl halide or with a fatty acid, respectively). Alternatively, the liposome may be fashioned in such a way that a connector portion is first incorporated into the membrane at the time of forming the membrane. The connector portion must have a lipophilic portion, which is firmly embedded and anchored in the membrane. It must also  
20 have a reactive portion, which is chemically available on the aqueous surface of the liposome. The reactive portion is selected so that it will be chemically suitable to form a stable chemical bond with the targeting agent or carbohydrate, which is added later. In some cases it is possible to attach the target agent to the connector molecule directly, but in most instances it is more suitable to use a third molecule to act as a chemical bridge, thus linking the connector  
25 molecule which is in the membrane with the target agent or carbohydrate which is extended, three dimensionally, off of the vesicle surface. The dosage ranges for the administration of the peptides of the invention are those large enough to produce the desired effect in which the symptoms of the immune response show some degree of suppression. The dosage should not be so large as to cause adverse side effects. Generally, the dosage will vary with the age,  
30 condition, sex and extent of the disease in the animal and can be determined by one of skill in

the art. The dosage can be adjusted by the individual physician in the event of any counterindications.

Additional pharmaceutical methods may be employed to control the duration of action. Controlled release preparations may be achieved by the use of polymers to conjugate, 5 complex or adsorb the peptide. The controlled delivery may be exercised by selecting appropriate macromolecules (for example, polyesters, polyamino carboxymethylcellulose, and protamine sulfate) and the concentration of macromolecules as well as the methods of incorporation in order to control release. Another possible method to control the duration of action by controlled release preparations is to incorporate the peptide into particles of a 10 polymeric material such as polyesters, polyamino acids, hydrogels, poly (lactic acid) or ethylene vinylacetate copolymers.

In order to protect peptides from binding with plasma proteins, it is preferred that the peptides be entrapped in microcapsules prepared, for example, by coacervation techniques or by interfacial polymerization, for example, hydroxymethylcellulose or gelatin-microcapsules 15 and poly (methymethacrylate) microcapsules, respectively, or in colloidal drug delivery systems, for example, liposomes, albumin microspheres, microemulsions, nanoparticles, and nanocapsules or in macroemulsions. Such teachings are disclosed in Remington's Pharmaceutical Sciences (16th Ed., A. Oslo, ed., Mack, Easton, Pa., 1980).

The peptides of the invention are well suited for use in targetable drug delivery 20 systems such as synthetic or natural polymers in the form of macromolecular complexes, nanocapsules, microspheres, or beads, and lipid-based systems including oil-in-water emulsions, micelles, mixed micelles, liposomes, and resealed erythrocytes. These systems are known collectively as colloidal drug delivery systems. Typically, such colloidal particles containing the dispersed peptides are about 50 nm-2  $\mu$ m in diameter. The size of the colloidal 25 particles allows them to be administered intravenously such as by injection, or as an aerosol. Materials used in the preparation of colloidal systems are typically sterilizable via filter sterilization, nontoxic, and biodegradable, for example albumin, ethylcellulose, casein, gelatin, lecithin, phospholipids, and soybean oil. Polymeric colloidal systems are prepared by a process similar to the coacervation of microencapsulation.

30 In an exemplary embodiment, the peptides are components of a liposome, used as a targeted delivery system. When phospholipids are gently dispersed in aqueous media, they

swell, hydrate, and spontaneously form multilamellar concentric bilayer vesicles with layers of aqueous media separating the lipid bilayer. Such systems are usually referred to as multilamellar liposomes or multilamellar vesicles (MLVs) and have diameters ranging from about 100 nm to about 4  $\mu$ m. When MLVs are sonicated, small unilamellar vesicles (SUVS) with diameters in the range of from about 20 to about 50 nm are formed, which contain an aqueous solution in the core of the SUV.

Examples of lipids useful in liposome production include phosphatidyl compounds, such as phosphatidylglycerol, phosphatidylcholine, phosphatidylserine, and phosphatidylethanolamine. Particularly useful are diacylphosphatidylglycerols, where the lipid moiety contains from 14-18 carbon atoms, particularly from 16-18 carbon atoms, and are saturated. Illustrative phospholipids include egg phosphatidylcholine, dipalmitoylphosphatidylcholine, and distearoylphosphatidylcholine.

In preparing liposomes containing the peptides of the invention, such variables as the efficiency of peptide encapsulation, lability of the peptide, homogeneity and size of the resulting population of liposomes, peptide-to-lipid ratio, permeability instability of the preparation, and pharmaceutical acceptability of the formulation should be considered. Szoka, et al, *Annual Review of Biophysics and Bioengineering*, 9: 467 (1980); Deamer, et al., in *LIPOSOMES*, Marcel Dekker, New York, 1983, 27; Hope, et al., *Chem. Phys. Lipids*, 40: 89 (1986)).

The targeted delivery system containing the peptides of the invention may be administered in a variety of ways to a host, particularly a mammalian host, such as intravenously, intramuscularly, subcutaneously, intra-peritoneally, intravascularly, topically, intracavitarily, transdermally, intranasally, and by inhalation. The concentration of the peptides will vary upon the particular application, the nature of the disease, the frequency of administration, or the like. The targeted delivery system-encapsulated peptide may be provided in a formulation comprising other compounds as appropriate and an aqueous physiologically acceptable medium, for example, saline, phosphate buffered saline, or the like.

The compounds prepared by the methods of the invention may also find use as diagnostic reagents. For example, labeled compounds can be used to locate areas of

inflammation or tumor metastasis in a patient suspected of having an inflammation. For this use, the compounds can be labeled with  $^{125}\text{I}$ ,  $^{14}\text{C}$ , or tritium.

## EXPERIMENTAL EXAMPLES

5 The invention is now described with reference to the following Examples. These Examples are provided for the purpose of illustration only and the invention should in no way be construed as being limited to these Examples, but rather should be construed to encompass any and all variations which become evident as a result of the teaching provided herein.

10 The materials and methods used in the experiments presented in this Example are now described.

### A. General Procedures

#### 1. Preparation of CMP-SA-PEG

15 This example sets forth the preparation of CMP-SA-PEG.

**Preparation of 2-(benzyloxycarboxamido)-glycylamido-2-deoxy-D-mannopyranose.** N-benzyloxycarbonyl-glycyl-N-hydroxysuccinimide ester (3.125 g, 10.2 mmol) was added to a solution containing D-mannosamine-HCl (2 g, 9.3 mmol) and triethylamine (1.42 mL, 10.2 mmol) dissolved in MeOH (10 mL) and H<sub>2</sub>O (6 mL). The reaction was stirred at room temperature for 16 hours and concentrated using rotoevaporation. Chromatography (silica, 10% MeOH/CH<sub>2</sub>Cl<sub>2</sub>) yielded 1.71 g (50% yield) of product as a white solid:  $R_f = 0.62$  (silica; CHCl<sub>3</sub>:MeOH:H<sub>2</sub>O, 6/4/1);  $^1\text{H}$  NMR (CD<sub>3</sub>OD, 500 MHz)  $\delta$  3.24-3.27 (m, 2H), 3.44 (t, 1H), 3.55 (t, 1H), 3.63-3.66 (m, 1H), 3.76-3.90 (m, 20 6H), 3.91 (s, 2H), 4.0 (dd, 2H), 4.28 (d, 1H,  $J = 4.4$ ), 4.41 (d, 1H,  $J = 3.2$ ), 5.03 (s, 1H), 5.10 (m, 3H), 7.29-7.38 (m, 10H).

**Preparation of 5-(N-benzyloxycarboxamido)glycylamido-3,5-dideoxy-D-glycero-D-galacto-2-nonulopyranosurionate.** 2-(N-Benzyloxycarboxamido) glycylamide-2-deoxy-D-mannopyranose (1.59 g, 4.3 mmol) was dissolved in a solution of 0.1 M HEPES (12 mL, pH 7.5) and sodium pyruvate (4.73 g, 43 mmol). Neuraminic acid aldolase (540 U of enzyme in 45 mL of a 10 mM phosphate buffered solution containing 0.1 M NaCl at pH 6.9) and the reaction mixture was heated to 37°C for 24 hr. The reaction mixture was then centrifuged

and the supernatant was chromatographed (C18 silica, gradient from H<sub>2</sub>O (100%) to 30% MeOH/water). Appropriate fractions were pooled, concentrated and the residue chromatographed (silica, gradient from 10% MeOH/ CH<sub>2</sub>Cl<sub>2</sub> to CH<sub>2</sub>Cl<sub>2</sub>/MeOH/ H<sub>2</sub>O 6/4/1). Appropriate fractions were collected, concentrated and the residue resuspended in water.

- 5 After freeze-drying, the product (1.67 g, 87% yield) was obtained as a white solid:  $R_f = 0.26$  (silica, CHCl<sub>3</sub>/MeOH/H<sub>2</sub>O 6/4/1); <sup>1</sup>H NMR (D<sub>2</sub>O, 500 MHz)  $\delta$  1.82 (t, 1H), 2.20 (m, 1H), 3.49 (d, 1H), 3.59(dd, 1H), 3.67-3.86 (m, 2H), 3.87(s, 2H), 8.89-4.05 (m, 3H), 5.16 (s, 2H), 7.45 (m, 5H).

**Preparation of 5-glycylamido-3,5-dideoxy-D-glycero-D-galacto-2-**

- 10 **nonulopyranosuronate.** 5-(N-Benzoyloxycarboxamido)glycylamido-3,5-dideoxy-D-glycero-D-galacto-2-nonulopyranosuronate (1.66 g, 3.6 mmol) was dissolved in 20 mL of 50% water/methanol. The flask was repeatedly evacuated and placed under argon and then 10% Pd/C (0.225 g) was added. After repeated evacuation, hydrogen (about 1 atm) was then added to the flask and the reaction mixture stirred for 18 hr. The reaction mixture was
- 15 filtered through celite, concentrated by rotary evaporation and freeze-dried to yield 1.24 g (100% yield) of product as a white solid:  $R_f = 0.25$  (silica, IPA/H<sub>2</sub>O/NH<sub>4</sub>OH 7/2/1); <sup>1</sup>H NMR (D<sub>2</sub>O, 500 MHz)  $\delta$  1.83 (t, 1H, J = 9.9), 2.23 (dd, 1H, J = 12.9, 4.69), 3.51-3.70 (m, 2H), 3.61(s, 2H), 3.75-3.84 (m, 2H), 3.95-4.06(m, 3H).

**Preparation of cytidine-5'-monophosphoryl-[5-(N-fluorenylmethoxy-**

- 20 **carboxamido)glycylamido-3,5-dideoxy- $\beta$ -D-glycero-D-galacto-2-nonulopyranosuronate].**

A solution containing 5-glycylamido-3,5-dideoxy-D-glycero-D-galacto-2-nonulopyranosuronate (0.55 g, 1.70 mmol) dissolved in 20 mL H<sub>2</sub>O was added to a solution of Tris (1.38 g, 11.4 mmol), 1 M MgCl<sub>2</sub> (1.1 mL) and BSA (55 mg). The pH of the solution was adjusted to 8.8 with 1M NaOH (2 mL) and CTP-2Na<sup>+</sup> (2.23 g, 4.2 mmol) was added.

- 25 The reaction mixture pH was controlled with a pH controller which delivered 1 M NaOH as needed to maintain pH 8.8. The fusion protein (sialyltransferase/CMP-neuraminic acid synthetase) was added to the solution and the reaction mixture was stirred at room temperature. After 2 days, an additional amount of fusion protein was added and the reaction stirred an additional 40 hours. The reaction mixture was precipitated in EtOH and the
- 30 precipitate was washed 5 times with cold EtOH to yield 2.3 grams of a white solid. About 1.0 g of the crude product was dissolved in 1,4 dioxane (4 mL), H<sub>2</sub>O (4 mL) and saturated

NaHCO<sub>3</sub> (3 mL) and a solution of FMOC-Cl (308 mg, 1.2 mmol) dissolved in 2 mL dioxane was added dropwise. After stirring for 16 hr at room temperature, the reaction mixture was concentrated to about 6 mL by rotary evaporation and purified using chromatography (C18 silica, gradient 100% H<sub>2</sub>O to 30% MeOH/ H<sub>2</sub>O). Appropriate fractions were combined and concentrated. The residue was dissolved in water and freeze-dried to yield 253 mg of a white solid:  $R_f = 0.50$  (silica, IPA/H<sub>2</sub>O/NH<sub>4</sub>OH 7/2/1); <sup>1</sup>H NMR (D<sub>2</sub>O, 500 MHz)  $\delta$  1.64 (dt, 1H,  $J = 12.0, 6.0$ ), 2.50 (dd, 1H,  $J = 13.2, 4.9$ ), 3.38 (d,  $J = 9.67, 1H$ ), 3.60 (dd,  $J = 11.65, 6.64, 1H$ ), 3.79 (d,  $J = 4.11, 1H$ ), 3.87 (dd,  $J = 12.24, 1.0, 1H$ ), 3.97 (m, 2H), 4.07 (td,  $J = 10.75, 4.84, 1H$ ), 4.17 (dd,  $J = 10.68, 1.0, 1H$ ), 4.25 (s, 2H), 4.32 (t,  $J = 4.4, 1H$ ), 4.37 (t,  $J = 5.8, 1H$ ), 4.6-4.7 (m, obscured by solvent peak), 5.95 (d,  $J = 4, 1H$ ), 6.03 (d,  $J = 7.4, 1H$ ), 7.43-7.53 (m, 3H), 7.74 (m, 2H), 7.94 (q,  $J = 7, 3H$ ). MS (ES); calc. for C<sub>35</sub>H<sub>42</sub>N<sub>5</sub>O<sub>18</sub>P ([M-H]<sup>-</sup>), 851.7; found 850.0.

**Preparation of cytidine-5'-monophosphoryl-(5-glycyamido-3,5-dideoxy- $\beta$ -D-glycero-D-galacto-2-nonulopyranosuronate).** Diisopropylamine (83  $\mu$ L, 0.587  $\mu$ mol) was added to a solution of cytidine-5'-monophosphoryl-[5-(N-fluorenyl-methoxycarboxamido)glycyamido-3,5-dideoxy- $\beta$ -D-glycero-D-galacto-2-nonulopyranosuronate] (100 mg, 0.117 mmol) dissolved in water (3 mL) and methanol (1 mL). The reaction mixture was stirred 16 hr at room temperature and the reaction methanol removed from the reaction mixture by rotary evaporation. The crude reaction mixture was filtered through a C18 silica gel column using water and the effluent was collected and freeze-dried to yield (87 mg, 100%) of product as a white solid:  $R_f = 0.21$  (silica, IPA/H<sub>2</sub>O/NH<sub>4</sub>OH 7/2/1); <sup>1</sup>H NMR (D<sub>2</sub>O, 500 MHz)  $\delta$  1.66 (td, 1H,  $J = 5.3$ ), 2.50 (dd, 1H,  $J = 13.2, 4.6$ ), 3.43 (d,  $J = 9.58, 1H$ ), 3.63 (dd,  $J = 11.9, 6.44, 1H$ ), 3.88 (dd,  $J = 11.8, 1.0, 1H$ ), 3.95 (td,  $J = 9.0, 2.3, 1H$ ), 4.10 (t,  $J = 10.42, 1H$ ), 4.12 (td,  $J = 10.34, 4.66, 1H$ ), 4.18 (d,  $J = 10.36, 1H$ ), 4.24 (m, 2H), 4.31 (t,  $J = 4.64, 1H$ ), 4.35 (t, 1H), 6.00 (d,  $J = 4.37, 1H$ ), 6.13 (d,  $J = 7.71, 1H$ ), 7.98 (d,  $J = 7.64, 1H$ ). MS (ES); calc. for C<sub>21</sub>H<sub>32</sub>N<sub>5</sub>O<sub>11</sub>P ([M-H]<sup>-</sup>), 629.47; found 627.9.

**Preparation of cytidine-5'-monophosphoryl-[5-(N-methoxy-polyoxyethylene-(1 kDa)-3-oxypropionamido)-glycyamido-3,5-dideoxy- $\beta$ -D-glycero-D-galacto-2-nonulopyranosuronate].** Benzyltriazol-1-yloxy-tris(dimethylamino)-phosphonium hexafluorophosphate (BOP, 21 mg, 48  $\mu$ mol) was added to a solution of methoxypolyoxyethylene-(1 kDa average molecular weight)-3-oxypropionic acid (48 mg, 48

μmol) dissolved in anhydrous DMF (700 μL) and triethylamine (13 μL, 95 μmol). After 30 min, a solution containing cytidine-5'-monophosphoryl-(5-glycylamido-3,5-dideoxy-β-D-glycero-D-galacto-2-nonulopyranosuronate) (30 mg, 48 μmol), water (400 μL) and triethylamine (13 μL, 95 μmol) was added. This solution was stirred 20 min at room temperature and then chromatographed (C18 silica, gradient of methanol/water). Appropriate fractions were collected, concentrated, the residue dissolved in water and freeze-dried to afford 40 mg (50% yield) of a white solid:  $R_f = 0.36$  (silica, IPA/H<sub>2</sub>O/NH<sub>4</sub>OH 7/2/1); <sup>1</sup>H NMR (D<sub>2</sub>O, 500 MHz) δ 1.66 (td, 1H, J=5.3), 2.50 (dd, 1H, J = 13.2, 4.6), 2.64 (t, J=5.99, 3H) 3.43 (d, J = 9.58, 1H), 3.63 (m, 1H), 3.71 (s, 70H), 3.79 (m, obscured by 3.71 peak), 3.82 (t, J=6.19, 1H) 3.88 (dd, J = 11.8, 1.0, 1H), 3.95 (td, J= 9.0, 2.3, 1H), 3.98 (t, J= 5.06, 1H), 4.12 (td, J = 10.34, 4.66, 1 H), 4.18 (d, J = 10.36, 1H), 4.23 (d, J=4.85, 2H), 4.31 (t, J=4.64, 1H), 4.35 (t, 1H), 6.00 (d, J = 4.55, 1 H), 6.13 (d, J = 7.56, 1H), 7.98 (d, J=7.54, 1H). MS (MALDI), observe [M- H]; 1594.5, 1638.5, 1682.4, 1726.4, 1770.3, 1814.4, 1858.2, 1881.5, 1903.5, 1947.3.

**Preparation of cytidine-5'-monophosphoryl-[5-(N-methoxy-polyoxyethylene-(10 kDa)-oxycarboxamido)-glycylamido-3,5-dideoxy-β-D-glycero-D-galacto-2-nonulopyranosuronate].** Cytidine-5'-monophosphoryl-(5-glycylamido-3,5-dideoxy-β-D-glycero-D-galacto-2-nonulopyranosuronate) (2.5 mg, 4 μmol) and water (180 μL) was added to a solution of (Methoxypolyoxyethylene-(10 kDa, average molecular weight)-oxycarbonyl-(N-oxybenzotriazole) ester (40 mg, 4 μmol) in anhydrous DMF (800 μL) containing triethylamine (1.1 μL, 8 μmol) and the reaction mixture stirred for 1 hr at room temperature. The reaction mixture was then diluted with water (8 mL) and was purified by reversed phase flash chromatography (C18 silica, gradient of methanol/water). Appropriate fractions were combined, concentrated, the residue dissolved in water and freeze-dried yielding 20 mg (46% yield) of product as a white solid:  $R_f = 0.35$  (silica, IPA/H<sub>2</sub>O/NH<sub>4</sub>OH 7/2/1); <sup>1</sup>H NMR (D<sub>2</sub>O, 500 MHz) δ 1.66 (td, 1H), 2.50 (dd, 1H), 2.64 (t, 3H) 3.55-3.7 (m, obscured by 3.71 peak), 3.71 (s, 488H), 3.72-4.0 (m, obscured by 3.71 peak), 4.23 (m, 3H), 4.31 (t, 1H), 4.35 (t, 1H), 6.00 (d, J = 4.77, 1 H), 6.12 (d, J = 7.52, 1H), 7.98 (d, J=7.89, 1H). MS (MALDI), observe [M- CMP+Na]; 10780.

## 2. Preparation of CMP-SA-PEG II

This example sets forth the general procedure for making CMP-SA-PEG, and specific procedures for making CMP-SA-PEG (1 kDa) and CMP-SA-PEG (20 kDa).

**General procedures Preparing Cytidine-5'-monophosphoryl-(5-glycyamido-3,5-dideoxy-β-D-glycero-D-galacto-2-nonulopyranosuronate).** Cytidine-5'-monophosphoryl-(5-glycyamido-3,5-dideoxy-β-D-glycero-D-galacto-2-nonulopyranosuronate) (870 mg, 1.02 mmol) was dissolved in 25 mL of water and 5.5 mL of 40 wt% dimethylamine solution in H<sub>2</sub>O was added. The reaction was stirred for 1 hr and the excess dimethyl amine was then removed by rotary evaporation. The aqueous solution was filtered through a C-18 silica gel column and the column was washed with water. The eluants were combined and lyophilized to afford 638 mg (93%) of a white solid.  $R_f = 0.10$  (silica, IPA/H<sub>2</sub>O/NH<sub>4</sub>OH; 7/2/1). <sup>1</sup>H NMR (D<sub>2</sub>O, 500 MHz) δ 1.66 (td, 1H, J=5.3), 2.50 (dd, 1H, J=13.2, 4.6), 3.43 (d, J=9.58, 1H), 3.63 (dd, J=11.9, 6.44, 1H), 3.88 (dd, J=11.8, 1.0, 1H), 3.95 (td, J=9.0, 2.3, 1H), 4.10 (t, J=10.42, 1H), 4.12 (td, J=10.34, 4.66, 1H), 4.18 (d, J=10.36, 1H), 4.24 (m, 2H), 4.31 (t, J=4.64, 1H), 4.35 (t, 1H), 6.00 (d, J=4.37, 1H), 6.13 (d, J=7.71, 1H), 7.98 (d, J=7.64, 1H). MS (ES); calc. for C<sub>21</sub>H<sub>32</sub>N<sub>5</sub>O<sub>11</sub>P ([M-H]<sup>-</sup>), 629.47; found 627.9.

**General procedures for Preparing CMP-SA-PEG using mPEG-(p-nitrophenol)carbonate.** Cytidine-5'-monophosphoryl-(5-glycyamido-3,5-dideoxy-β-D-glycero-D-galacto-2-nonulopyranosuronate) (175 mg, 0.259 mMol) was dissolved in a mixture of water, pH 8.5, and DMF or THF (in a ratio of 1:2). The mPEG-nitrophenol carbonate (2 to 20 kDa mPEG's) (0.519 mMole) was added in several portions over 8 hr at room temperature and the reaction mixture was stirred at room temperature for 3 days. When complete, water (40 ml) and 1.5 ml of NH<sub>4</sub>OH (29% aqueous solution) were added. The yellow reaction mixture was stirred for another 2 hr and then concentrated by rotary evaporation. The reaction mixture was then diluted with water (pH 8.5) to about 500 ml volume and was purified by reversed phase flash chromatography (Biotage 40M, C18 silica column) with a gradient of methanol/water. Appropriate fractions were combined and concentrated to afford the products as white solids.  $R_f$  (silica; 1-propanol / water / 29%NH<sub>4</sub>OH; 7 / 2 / 1); (2 kDa PEG) = 0.31; (5 kDa PEG) = 0.33; (10 kDa PEG) = 0.36; (20 kDa PEG) = 0.38 (TLC silica, IPA/H<sub>2</sub>O/NH<sub>4</sub>OH 7/2/1); MS (MALDI), observe [M-CMP+Na<sup>+</sup>]; (2 kDa) = 2460; (5 kDa) = 5250; (10 kDa) = 10700; (20 kDa) = 22500.

**Preparation of Cytidine-5'-monophosphoryl-[5-(N-fluorenylmethoxycarboxamido)-glycylamido-3,5-dideoxy-β-D-glycero-D-galacto-2-nonulopyranosuronate].** Sodium pyruvate (2.4 g, 218 mmol), HEPES buffer (0.25 M, pH 7.34) and 1.0 g (22 mmol) of Fmoc-glycylmannosamide were mixed in a 150 mL

polycarbonate bottle. A neuraminic acid aldolase solution (19 mL, ~ 600 U) was then added and the reaction mixture was incubated at 30 °C on an orbital shaker. After 23 hours, Thin layer chromatography (TLC) indicated that approximately 75% conversion to product had occurred. The CTP (1.72 g, 33 mmol) and 0.1 M of MnCl<sub>2</sub> (6 mL) were then added to the reaction mixture. The pH was adjusted to 7.5 with 1 M NaOH (5.5 mL) and a solution containing CMP-neuraminic acid synthetase (*Neisseria*) was added (25 mL, 386 U). The reaction was complete after 24 hrs and the reaction mixture was chromatographed (C-18 silica, gradient from H<sub>2</sub>O (100%) to 10% MeOH/H<sub>2</sub>O). Appropriate fractions were recombined, concentrated and lyophilized to afford a white solid, R<sub>f</sub> (IPA/ H<sub>2</sub>O/NH<sub>4</sub>OH, 7/2/1) = 0.52. <sup>1</sup>H NMR (D<sub>2</sub>O, 500 MHz) δ 1.64 (dt, 1H, J = 12.0, 6.0), 2.50 (dd, 1H, J = 13.2, 4.9), 3.38 (d, J = 9.67, 1H), 3.60 (dd, J=11.65, 6.64, 1H), 3.79 (d, J=4.11, 1H), 3.87 (dd, J= 12.24, 1.0, 1H), 3.97 (m, 2H), 4.07 (td, J = 10.75, 4.84, 1H), 4.17 (dd, J = 10.68, 1.0, 1 H), 4.25 (s, 2H), 4.32 (t, J = 4.4, 1H), 4.37 (t, J=5.8 1H), 4.6-4.7 (m, obscured by solvent peak), 5.95 (d, J = 4, 1 H), 6.03 (d, J = 7.4, 1H), 7.43-7.53 (m, 3H), 7.74 (m, 2H), 7.94 (q, J = 7, 3H). MS (ES); calc. for C<sub>35</sub>H<sub>42</sub>N<sub>5</sub>O<sub>18</sub>P ([M-H]<sup>-</sup>), 850.7; found 850.8.

**Preparation of Cytidine-5'-monophosphoryl-[5-(N-methoxypolyoxyethylene-(1 kDa)-3-oxypropionamido)-glycylamido-3,5-dideoxy-β-D-glycero-D-galacto-2-nonulopyranosuronate].** Methoxypolyoxyethylene-(1 kDa average molecular weight)-3-oxypropionate-N-succinimidyl ester (52 mg, 52 μmol) dissolved in anhydrous DMF (450 μL) and triethylamine (33 μL, 238 μmol). Cytidine-5'-monophosphoryl-(5-glycylamido-3,5-dideoxy-β-D-glycero-D-galacto-2-nonulopyranosuronate) (30 mg, 48 μmol) was added as a solid. Water, pH 8 (330 μL) was added and after 30 min, an additional 28 mg of NHS-activated PEG was added. After an additional 5 min, the reaction mixture was chromatographed (C-18 silica, gradient of methanol/water), and appropriate fractions were concentrated to afford 32 mg (40% yield) of a white solid, R<sub>f</sub> = 0.31 (silica, IPA/H<sub>2</sub>O/NH<sub>4</sub>OH 7/2/1); <sup>1</sup>H NMR (D<sub>2</sub>O, 500 MHz) δ 1.66 (td, 1H, J = 5.3), 2.50 (dd, 1H, J = 13.2, 4.6), 2.64 (t,

J=5.99, 3H) 3.43 (d, J = 9.58, 1H), 3.63 (m, 1H), 3.71 (s, 70H), 3.79 (m, obscured by 3.71 peak), 3.82 (t, J=6.19, 1H) 3.88 (dd, J = 11.8, 1.0, 1H), 3.95 (td, J= 9.0, 2.3, 1H), 3.98 (t, J= 5.06, 1H), 4.12 (td, J = 10.34, 4.66, 1 H), 4.18 (d, J = 10.36, 1H), 4.23 (d, J=4.85, 2H), 4.31 (t, J=4.64, 1H), 4.35 (t, 1H), 6.00 (d, J = 4.55, 1 H), 6.13 (d, J = 7.56, 1H), 7.98 (d, J=7.54, 1H). MS (MALDI), observe [(M-CMP)-H]; 1506.4, 1550.4, 1594.5, 1638.5, 1682.4, 1726.4, 1770.3, 1814.4, 1858.2.

**Preparation of Cytidine-5'-monophosphoryl-{5-[N-(2,6-dimethoxypolyoxyethylene-(20 kDa)-3oxypropionamidyl-lysylamido]-glycylamido-3,5-dideoxy-β-D-glycero-D-galacto-2-nonulopyranosurionate}**. The 2,6-Di-[methoxypolyoxyethylene-(20 kDa average molecular weight)-3-oxypropionamidyl]-lysylamido-N-succinimidyl ester (367 mg, 9 μmol) was dissolved in anhydrous THF (7 mL) and triethylamine (5 μL, 36 μmol). Cytidine-5'-monophosphoryl-(5-glycylamido-3,5-dideoxy-β-D-glycero-D-galacto-2-nonulopyranosurionate) (30 mg, 48 μmol) was dissolved in 1.0 mL of water, and added to the reaction mixture. The reaction was stirred for 4 hours at room temperature and was then chromatographed (HPLC, Waters Xterra RP8, gradient from water/NH<sub>4</sub>OH, 100% to 20% methanol/water/NH<sub>4</sub>OH at 1 mL/min) to afford a white solid with a R<sub>t</sub> = 22.8 min. MS (MALDI), observe [(M-CMP)-H]; 43027.01 (40,000 – 45,500).

### 3. Preparation of UDP-Gal-PEG.

This example sets forth the general procedure for making UDP-Gal-PEG. Methoxypolyoxyethylenepropionate N-hydroxysuccinimide ester (mPEG-SPA, MW 1,000) 348 mg in THF (0.5 mL) was added to a solution of 25 mg of galactosamine-1-phosphate in 1 ml of water, followed by the addition of 67 μL triethylamine. The resulting mixture was stirred at room temperature for 17 hr. Concentration at reduce pressures provided a crude reaction mixture which was purified by chromatography (C-18 silica, using a step gradient of 10%, 20%, 30%, 40% aqueous MeOH) to afford 90 mg (74%) of product after the appropriate fractions were combined and concentrated to dryness. R<sub>f</sub> = 0.5 (silica, Propanol/H<sub>2</sub>O/NH<sub>4</sub>OH 30/20/2); MS(MALDI), observed 1356, 1400, 1444, 1488, 1532, 1576, 1620.

**[ $\alpha$ -1-(Uridine-5'-diphosphoryl)]-2-deoxy-2-(methoxypolyoxyethylene-propionoylamido-1 kDa)- $\alpha$ -D-galactosamine.** The 2-deoxy-2-(methoxypolyoxyethylenepropionoylamido-1 kDa)- $\alpha$ -1-monophosphate-D-galactosamine (58 mg) was dissolved in 6 mL of DMF and 1.2 mL of pyridine. UMP-morpholidate (60 mg) was then added and the resulting mixture was stirred at 70°C for 48 hr. After concentration, the residue was chromatographed (C18-silica, using a step gradient of 10%, 20%, 30%, 40%, 50%, 80% MeOH) to yield 50 mg of product after concentration of the appropriate fractions.  $R_f$  = 0.54 (silica, propanol/H<sub>2</sub>O/NH<sub>4</sub>OH 30/20/2). MS(MALDI); Observed 1485, 1529, 1618, 1706.

**[ $\alpha$ -1-(Uridine-5'-diphosphoryl)]-6-deoxy-6-(methoxypolyoxyethylene-amino-2 kDa)- $\alpha$ -D-galactose.** [ $\alpha$ -1-(Uridine-5'-diphosphoryl)]-6-carboxaldehyde- $\alpha$ -D-galactose (10 mg) was dissolved in 2 mL of 25 mM sodium phosphate buffer (pH 6.0) and treated with methoxypolyethyleneglycol amine (MW 2,000, 70 mg) and then 25  $\mu$ L of 1M NaBH<sub>3</sub>CN solution at 0°C. The resulting mixture was frozen at -20°C for three days. The reaction mixture was chromatographed (HPLC, Water Xterra P8) using 0.015 M NH<sub>4</sub>OH as mobile phase A and MeOH as mobile phase B as eluent at the speed of 1.0 mL/min. The product was collected, concentrated to yield a solid;  $R_t$  = 9.4 minutes.  $R_f$  = 0.27 (silica, EtOH/H<sub>2</sub>O 7/3).

**[ $\alpha$ -1-(Uridine-5'-diphosphoryl)]-6-amino-6-deoxy- $\alpha$ -D-galactose.** Ammonium acetate 15 mg was added to a solution of [ $\alpha$ -1-(Uridine-5'-diphosphoryl)]-6-carboxaldehyde- $\alpha$ -D-galactopyranoside (10 mg) in sodium phosphate buffer (pH 6.0). A solution of (25  $\mu$ L) 1M NaBH<sub>3</sub>CN was then added and the mixture was stirred for 24 hr. The solution was concentrated and the residue was chromatographed (sephadex G<sub>10</sub>) to afford 10 mg of a white solid,  $R_f$  = 0.62 (silica, EtOH/0.1 M NH<sub>4</sub>Ac).

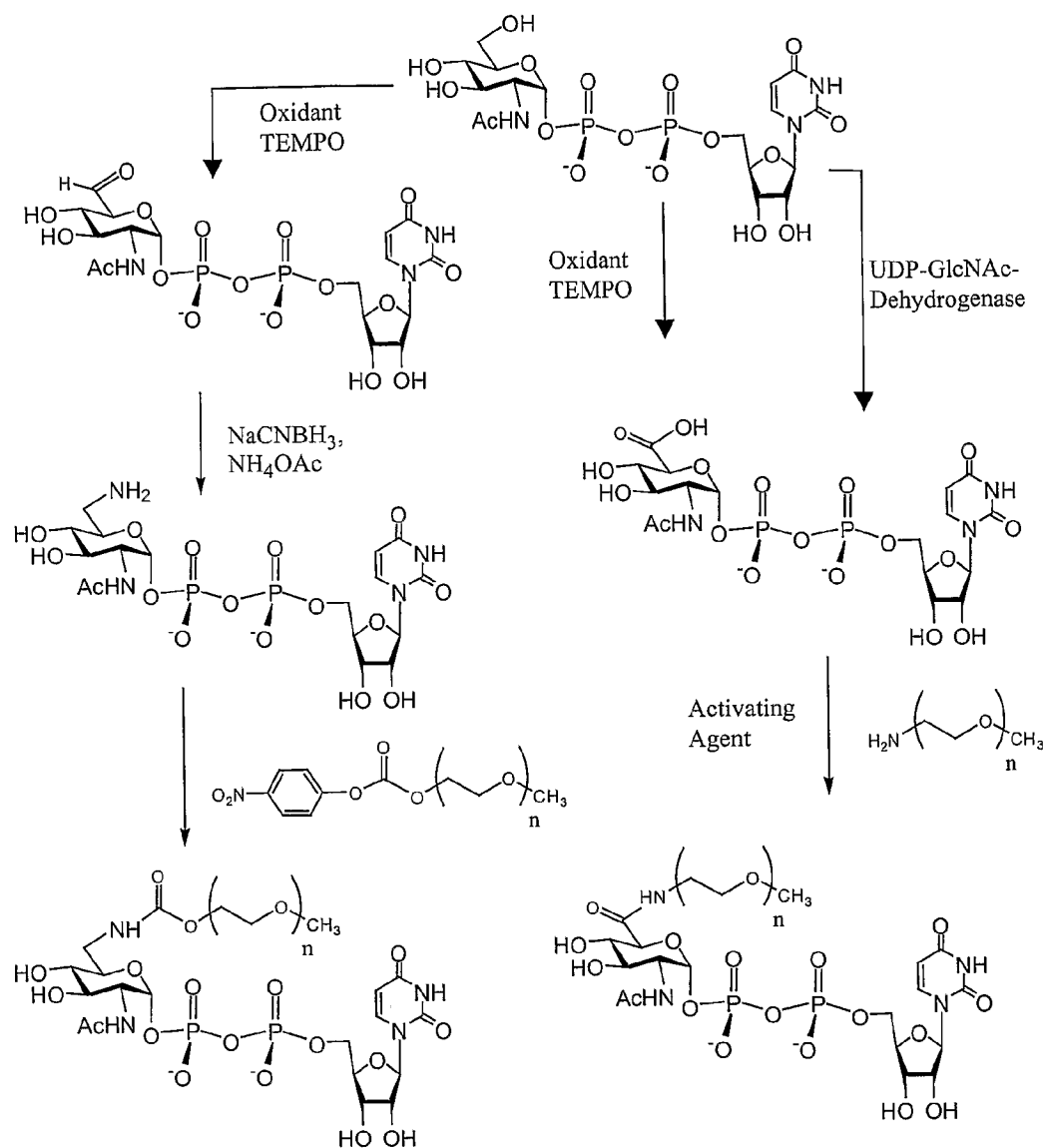
**[ $\alpha$ -1-(Uridine-5'-diphosphoryl)]-6-deoxy-6-(methoxypolyoxyethylenepropionoylamido, ~2 kDa)- $\alpha$ -D-galactopyranoside.** [ $\alpha$ -1-(Uridine-5'-diphosphoryl)]-6-amino-6-deoxy- $\alpha$ -D-galactopyranoside (5 mg) was dissolved in 1 mL of H<sub>2</sub>O. Then methoxypolyethyleneglycolpropionoyl-NHS ester (MW ~2,000, 66 mg) was added, followed by 4.6  $\mu$ L triethylamine. The resulting mixture was stirred at room temperature overnight, and then purified on HPLC (C-8 silica) to afford the product,  $R_t$  = 9.0 min.

**[ $\alpha$ -1-(Uridine-5'-diphosphoryl)]-6-deoxy-6-(methoxypolyoxyethylenecarboxamido, ~2 kDa)- $\alpha$ -D-galactopyranoside.** [ $\alpha$ -1-(Uridine-5'-diphosphoryl)]-6-amino-6-deoxy- $\alpha$ -D-galactopyranoside (10 mg) was mixed with methoxypolyethyleneglycolcarboxy-HOBT (MW 2000, 67 mg) in 1 mL of H<sub>2</sub>O, followed by the addition of EDC(1-ethyl-3-(3-dimethylaminopropyl)carbodiimide hydrochloride 6.4 mg and 4.6  $\mu$ L triethylamine. The resulting mixture was stirred at room temperature 24 hr. The mixture was chromatographed (C-8 silica) to afford the product.

#### 4. Preparation of UDP-GlcNAc-PEG

10        This example sets forth the general procedure for making UDP-GlcNAc-PEG. On the left side of scheme 17, the protected amino sugar diphospho-nucleotide is oxidized to form an aldehyde at the 6-position of the sugar. The aldehyde is converted to the corresponding primary amine by formation and reduction of the Schiff base. The resulting adduct is contacted with the p-nitrophenol carbonate of m-PEG, which reacts with the amine, 15 binding the m-PEG to the saccharide nucleus via an amide bond. On the right side of scheme 17 at the top, the protected amino sugar diphospho-nucleotide is treated with a chemical oxidant to form a carboxyl group at the 6-carbon of the sugar nucleus. The carboxyl group is activated and reacted with m-PEG amine, binding the m-PEG to the saccharide nucleus via an amide bond. On the right side of scheme 17 at the bottom the reactions are substantially 20 similar to that on the top right, with the exception that the starting sugar nucleotide is contacted with an oxidizing enzyme, such as a dehydrogenase, rather than a chemical oxidant.

Scheme 17.

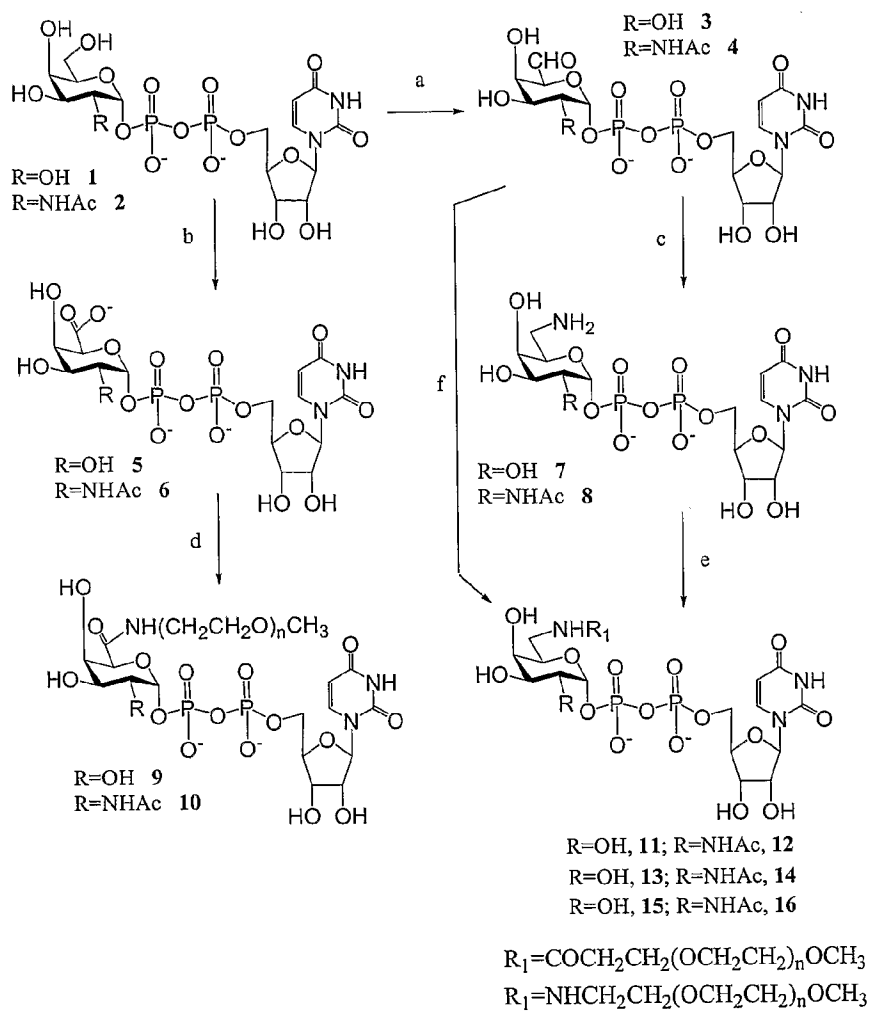


### 5. Preparation of UDP-GalNAc-PEG

- 5 This example (scheme 18) sets forth the general procedure for making UDP-GalNAc-PEG. The reaction set forth above originates with a sugar diphospho-nucleotide, in which R is either a hydroxyl **1** or a protected amine **2**. In step a, the starting sugar is treated with a mixture of an oxidase and a catalase, converting the 6-position of the sugar into an aldehyde moiety (**3** and **4**). In step c, the aldehyde is converted to the corresponding amine (**7** and **8**)

by formation and reduction of a Schiff base. In step e, the amine is optionally treated with an activated m-PEG derivative, thereby acylating the amine to produce the corresponding m-PEG amide (**11** and **13**). Alternatively, in step f, the amine is contacted with an activated m-PEG species, such as a m-PEG active ester, thereby forming the corresponding m-PEG amide  
5 (**12** and **14**). In step b, the starting material is also treated with a catalase and oxidase, completely oxidizing the hydroxymethyl moiety, forming a carboxyl group at the 6-position. In step d, the carboxyl moiety is activated and subsequently converted to a m-PEG adduct (**9** and **10**) by reaction with a m-PEG amine intermediate. This is shown in scheme 18.

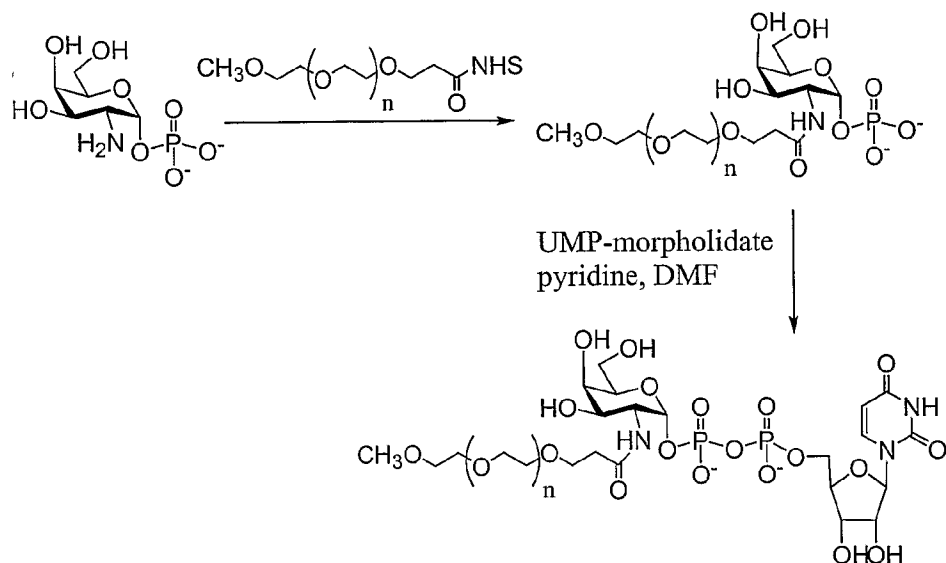
Scheme 18.



a and b): Galactose oxidase and catalase in 25 mM sodium phosphate buffer (pH 6.0); c):  $NH_4Ac$ ,  $NaBH_3CN$  in 25 mM sodium phosphate buffer (pH 6.0); d)  $CH_3(OCH_2CH_2)NH_2$ , EDC,  $H_2O$ ; e).  $CH_3(OCH_2CH_2)_nNH_2$ ,  $NaBH_3CN$ ,  $H_2O$  for 15 and 16; f)  $CH_3O(CH_2CH_2O)_nCH_2CH_2CONHS$ ,  $H_2O$ ,  $Et_3N$

The amino-sugar phosphate is contacted with a m-PEG N-hydroxy succinimide active ester, thereby forming the corresponding sugar-PEG-amide. The amide is contacted with UMP-morpholidate to form the corresponding active sugar diphospho-nucleotide.

5 **Scheme 19.**



**6. Synthesis of CMP-SA-Levulinate**

This example sets forth the procedure for the synthesis of CMP-SA-levulinate.

- 10 **Preparation of 2-levulinamido-2-deoxy-D-mannopyranose.** Isobutylchloroformate (100  $\mu$ L, 0.77 mmol) was added dropwise to a solution of levulinic acid (86  $\mu$ L, 0.84 mmol), anhydrous THF (3 mL) and triethylamine (127  $\mu$ L, 0.91 mmol). This solution was stirred for 3 hours at room temperature and was then added dropwise to a solution containing D-mannosamine hydrochloride (151 mg, 0.7 mmol), triethylamine (127  $\mu$ L, 0.91 mmol), THF
- 15 (2 mL) and water (2 mL). The reaction mixture was stirred 15 hours and then concentrated to dryness by rotary evaporation. Chromatography (silica, step gradient of 5-15% MeOH/CH<sub>2</sub>Cl<sub>2</sub>) was used to isolate the product yielding 0.156 g (73% yield) of a white solid:  $R_f$  = 0.41 (silica, CHCl<sub>3</sub>/MeOH/water 6/4/1); <sup>1</sup>H NMR (D<sub>2</sub>O, 500 MHz)  $\delta$  2.23 (s, 3H), 2.24 (s, 3H), 2.57(td, J = 6.54, 3.68, 2H) 2.63 (t, J=6.71, 2H), 2.86-2.90 (m, 4H), 3.42 (m, 1H),
- 20 3.53 (t, J=9.76, 1H), 3.64 (t, J=9.43, 1H), 3.80-3.91 (m, 4H), 4.04 (dd, J = 9.79, 4.71, 1 H),

4.31 (dd, J = 4.63, 1.14, 1H), 4.45 (dd, J = 4.16, 1.13, 1H), 5.02 (d, J = 1.29, 1H), 5.11 (s, J = 1.30, 1H), MS (ES); calculated for C<sub>11</sub>H<sub>19</sub>NO<sub>7</sub>, 277.27; found [M+1] 277.9.

**Preparation of 5-levulinamido-3,5-dideoxy-D-glycero-D-galacto-2-**

**nonulopyranosuronate.** Sodium pyruvate (0.616 g, 5.6 mmol) and N-acetylneuraminic acid

5 aldolase (50 U) was added to a solution of 2-levulinamido-2-deoxy-D-mannopyranose (0.156 g, 0.56 mmol) in 0.1 M HEPES (pH 7.5). The reaction mixture was heated to 37 °C for 20 hours and after freezing. The reaction mixture was then filtered through C18 silica, frozen and freeze-dried. The crude solid was purified using flash chromatography (silica, first using 10-40% MeOH/CH<sub>2</sub>Cl<sub>2</sub> and then CH<sub>2</sub>Cl<sub>2</sub>/MeOH/H<sub>2</sub>O 6/4/0.5). Appropriate fractions were  
10 combined and concentrated yielding 45 mg (80% yield) of a white solid: R<sub>f</sub> = 0.15 (silica, CHCl<sub>3</sub>/MeOH/water 6/4/1); <sup>1</sup>H NMR (D<sub>2</sub>O, 500 MHz) δ 1.82 (t, J = 11.9, 1H), 2.21 (dd, J = 13.76, 4.84, 1H), 2.23 (s, 3H), 2.57 (app q, J = 6.6, 2H), 2.86-2.95 (m, 2H), 3.15-3.18 (m, 1H), 3.28-3.61 (complex, 1H), 3.60 (dd, J = 11.91, 6.66, 1H), 3.75 (td, J = 6.65, 2.62, 1H), 3.84 (dd, J = 11.89, 2.65, 1H), 3.88-4.01 (complex, 2H), 4.04 (td, J = 11.18, 4.67, 1H), MS (ES);  
15 calculated for C<sub>14</sub>H<sub>23</sub>NO<sub>10</sub>, 365.33; found ([M-1]<sup>-</sup>), 363.97.

**Preparation of cytidine-5'-monophosphoryl-(5-levulinamido-3,5-dideoxy-β-D-glycero-D-galacto-2-nonulopyranosuronate).** 5-Levulinamido-3,5-dideoxy-D-glycero-D-galacto-2-nonulopyranosuronate (50 mg, 137 μmol) was dissolved in 2 mL of 100 mM HEPES pH 7.5 buffer and 1 M MnCl<sub>2</sub> (300 μL, 300 μmol) was added. CTP-2Na<sup>+</sup> (79 mg,  
20 1.5 μmol) was dissolved in 5 mL HEPES buffer and was added to the sugar. The sialyltransferase/CMP-neuraminic acid synthetase fusion enzyme (11 U) was added and the reaction mixture stirred at room temperature for 45 hours. The reaction mixture was filtered through a 10,000 MWCO filter and the filtrate, which contained the product of the reaction, was used directly without further purification: R<sub>f</sub> = 0.35 (silica, IPA/water/NH<sub>4</sub>OH 7/2/1).

25

**B. Glycoconjugation and GlycoPEGylation of Peptides**

**α-Protease Inhibitor (α-Antitrypsin)**

**7. Sialylation of Recombinant Glycoproteins Antithrombin III, Fetuin and α1-Antitrypsin**

30 This example sets forth the preparation of sialylated forms of several recombinant peptides.

**Sialylation of Recombinant Glycoproteins Using ST3Gal III.** Several glycoproteins were examined for their ability to be sialylated by recombinant rat ST3Gal III. For each of these glycoproteins, sialylation will be a valuable process step in the development of the respective glycoproteins as commercial products.

- 5        **Reaction Conditions.** Reaction conditions were as summarized in Table 11. The sialyltransferase reactions were carried out for 24 hour at a temperature between room temperature and 37°. The extent of sialylation was established by determining the amount of <sup>14</sup>C-NeuAc incorporated into glycoprotein-linked oligosaccharides. See Table 11 for the reaction conditions for each protein.

10        **Table 11.** Reaction conditions.

Protein	Source	Protein Total (mg)	Protein Conc. (mg/ml)	ST (mU/mL)	ST/Protein (mU/mg)	CMP- NeuAc of "cycle" <sup>1</sup>
ATIII	Genzyme Transgenics	8.6	4.3	210	48	cycle
ATIII	Genzyme Transgenics	860	403	53	12	cycle
Asialo- fetuin	Sigma	0.4	105	20	13	10 mM
asialo- AAAT	PPL	0.4	0.5	20	20	20 mM

<sup>1</sup> "Cycle" refers to generation of CMP-NeuAc "in situ" enzymatically using standard conditions as described in specification (20 mM NeuAc and 2 mM CMP). The buffer was 0.1 M HEPES, pH 7.5.

- 15        The results presented in Table 12 demonstrate that a remarkable extent of sialylation was achieved in every case, despite low levels of enzyme used. Essentially, complete sialylation was obtained, based on the estimate of available terminal galactose. Table 12 shows the results of the sialylation reactions. The amount of enzyme used per mg of protein (mU/mg) as a basis of comparison for the various studies. In several of the examples shown,
- 20        only 7-13 mU ST3Gal III per mg of protein was required to give essentially complete sialylation after 24 hours.

**Table 12.** Analytical results

Protein	Source	Terminal Gal <sup>1</sup> mol/mol	NeuAc Incorp. <sup>2</sup> mol/mol	% Rxn <sup>3</sup>	Other characterization
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ATIII <sup>4</sup>	Genzyme	102	104	117	None
	Transgenics				
ATIII <sup>4</sup>	Genzyme	102	1.3	108	SDS-gels: protein purity
	Transgenics				FACs: carbohydrate glycoforms
Asialo-fetuin	Sigma	802	905	116	None
asialo-AAAT <sup>5</sup>	PPL	7	7.0	100	SDS-gels: protein purity

<sup>1</sup> Terminal (exposed) Gal content on N-linked oligosaccharides determined by supplier, or from literatures values (fetuin, asialo-AAAT).

<sup>2</sup> NeuAc incorporated determined by incorporation of <sup>14</sup>C-NeuAc after separation from free radiolabeled precursors by gel filtration.

5 <sup>3</sup> The % Rxn refers to % completion of the reaction based on the terminal Gal content as a theoretical maximum.

<sup>4</sup> Antithrombin III.

<sup>5</sup>  $\alpha$ 1 Antitrypsin.

10 These results are in marked contrast to those reported in detailed studies with bovine ST6Gal I where less than 50 mU/mg protein gave less than 50% sialylation, and 1070 mU/mg protein gave approximately 85-90% sialylation in 24 hours. Paulson et al. (1977) J. Biol. Chem. 252: 2363-2371; Paulson et al. (1978) J. Biol. Chem. 253: 5617-5624. A study of rat  $\alpha$ 2,3 and  $\alpha$ 2,6 sialyltransferases by another group revealed that complete sialylation of asialo-  
15 AGP required enzyme concentrations of 150-250 mU/mg protein (Weinstein et al. (1982) J. Biol. Chem. 257: 13845-13853). These earlier studies taken together suggested that the ST6Gal I sialyltransferase requires greater than 50 mU/mg and up to 150 mU/mg to achieve complete sialylation.

This Example demonstrates that sialylation of recombinant glycoproteins using the  
20 ST3 Gal III sialyltransferase required much less enzyme than expected. For a one kilogram scale reaction, approximately 7,000 units of the ST3Gal III sialyltransferase would be needed, instead of 100,000-150,000 units that earlier studies indicated. Purification of these enzymes from natural sources is prohibitive, with yields of only 1-10 units for a large scale preparation after 1-2 months work. Assuming that both the ST6Gal I and ST3Gal III  
25 sialyltransferases are produced as recombinant sialyltransferases, with equal levels of expression of the two enzymes being achieved, a fermentation scale 14-21 times greater (or more) would be required for the ST6Gal I sialyltransferase relative to the ST3Gal III

sialyltransferase. For the ST6Gal I sialyltransferase, expression levels of 0.3 U/l in yeast has been reported (Borsig et al. (1995) Biochem. Biophys. Res. Commun. 210: 14-20).

Expression levels of 1000 U/liter of the ST3 Gal III sialyltransferase have been achieved in *Aspergillus niger*. At current levels of expression 300-450,000 liters of yeast fermentation would be required to produce sufficient enzyme for sialylation of 1 kg of glycoprotein using the ST6Gal I sialyltransferase. In contrast, less than 10 liter fermentation of *Aspergillus niger* would be required for sialylation of 1 kg of glycoprotein using the ST3Gal III sialyltransferase. Thus, the fermentation capacity required to produce the ST3Gal III sialyltransferase for a large scale sialylation reaction would be 10-100 fold less than that required for producing the ST6Gal I; the cost of producing the sialyltransferase would be reduced proportionately.

### Cri-IgG Antibody

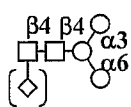
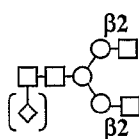
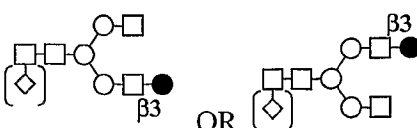
#### 8. Glyco-Remodeling of Cri-IgG1 Antibodies

This example sets forth the procedures for *in vitro* remodeling of Cri-IgG1 antibodies.

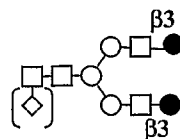
N-glycosylation at one conserved site at Asn 297 in the Fc domain of a monoclonal antibody can modulate its pharmacokinetic behavior and effector functions (Dwek et al., 1995, J. Anat. 187:279-292; Boyd et al., 1995, Mol. Immunol. 32:1311-1318; Lund et al., 1995, FASEB J. 1995, 9:115-119; Lund et al., 1996, J. Immunol. 157:4963-4969; Wright & Morrison, 1998, J. Immunol. 160:3393-3402; Flynn & Byrd, 2000, Curr. Opin. Oncol. 12:574-581). During cell culture fermentation or in certain pathological conditions, significant heterogeneity arises in the glycosylation pattern at this site. The resulting different patterns of glycosylation on the Fc domain are characterized by complex biantennary structures with zero, one, and two terminal galactose residues (G0, G1, and G2, respectively, see Table 13). The observed glycoform variations, such as the variation in terminal galactosylation, truncated N-glycoforms and bisecting modification, have been shown to influence the antibody's therapeutic properties, especially its ability to mediate targeted cell killing through complement binding and activation (Boyd et al., 1995, *supra*; Wright & Morrison, 1998, *supra*, Mimura et al., 2000, Molec. Immunol. 37:697-706; Davies et al., 2001, Biotechnol. Bioeng. 74:288-294).

In order to obtain different glycoforms of Cri-IgG1 antibodies and test their Fc effector functions, Cri-IgG1 antibodies were trimmed back stepwise using exoglycosidases to generate glycoforms lacking sialic acid (G2, G1), glycoforms lacking sialic acid and galactose (G0), and glycoforms lacking sialic acid, galactose and N-acetyl glucosamine (M3N2F), as illustrated in Table 13. These molecules were subsequently modified using different glycosyltransferases and appropriate sugars. Modification conditions were developed that resulted in the conversion of the original antibody glycan structures into different glycoforms: M3N2, GnT-I-M3N2 (the M3M2 glycoform with a GlcNAc moiety added using GnT-I), G0, Bisecting-G0 (the G0 moiety with a bisecting GlcNAc added with GnT-III), galactosylated bisecting-G0 (the bisecting-G0 glycoform with terminal galactose moieties added), G2, mono-sialylated S1( $\alpha$ 2,6)-G2 (the G2 glycoform with one terminal sialic acid moiety added using  $\alpha$ 2,6-sialyltransferase), S1( $\alpha$ 2,3)-G2 (the G2 glycoform with one terminal sialic acid moiety added using  $\alpha$ 2,3-sialyltransferase) and disialylated S2( $\alpha$ 2,3)-G2 (the G2 glycoform). After every glycoremodeling step, the glycan structures were enzymatically released from the antibody protein and were analyzed by various methods, including separation by capillary electrophoresis, 2-AA HPLC profiling and MALDI-TOF mass spectrometry.

**Table 13.** Abbreviations for glycoform structures.

Abbreviation	Glycan Structure(s)
M3N2(F)	
G0	
G1	

G2




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◇ = fucose, □ = GlcNAc, ○ = mannose, ● = galactose

The materials and methods used in these experiments are now described.

The Cri-IgG1 Monoclonal Antibody. The Cri-IgG1 antibody was obtained from R. Jefferies, MRC Center for Immune Regulation, The Medical School, University of Birmingham, UK. The antibody is a non-recombinant antibody, and is isolated from a human myeloma. The antibody was prepared using three methods. In the first method, referred to as “DEAE,” the antibody was isolated under relatively mild conditions using a DEAE ion exchange column. In the second method, referred to as “SPA,” the antibody was purified on a protein A column (*Staphylococcus aureus* protein A) with a low pH elution step. In the third method, referred to as “Fc,” the antibody was treated with a protease so that only the Fc portion of the antibody remained and the antigen binding domains were removed. These methods for antibody purification are well known to those of skill in the art and are not repeated in detail here.

**Affinity purification of remodeled antibodies.** Antibody, modified either by exoglycosidase or glycosyltransferase, was affinity purified on a ProA-sepharose 4-fast flow column (Amersham Bioscience, Arlington Heights, IL), eluted with 0.1 M glycine-HCl buffer, pH 2.7, and immediately neutralized with 1 M Tris, pH 9.5. The eluates were buffer-exchanged using a NAP-10 column (Amersham Bioscience, Arlington Heights, IL) to an appropriate buffer for the next step of glycosylation, such as 100 mM MES, pH 6.5 or 50 mM Tris-HCl, pH 7.2. The remodeled final products were dialyzed extensively against PBS at 4°C in Tube-O-Dialyzers™ (Chemicon International, Temecula, CA) with a MWCO of 8 kDa.

In vitro glycosidase treatment of Cri-antibodies. Antibody was buffer-exchanged into 50 mM Na phosphate/Citrate, pH 6.0 using NAP-10 column (Amersham Bioscience, Arlington Heights, IL). *In vitro* trimming back of sugar moieties was carried out stepwise, by contacting the antibody (5 mg/mL) with 20 mU/mg protein neuraminidase at 37°C overnight

(to remove terminal sialic acid moieties ), 20 mU/mg protein  $\beta$ -galactosidase at 37°C, overnight (to remove terminal galactose moieties to result in the G0 glycoform), and/or 2 U/mg  $\beta$ -N-acetylhexosaminidase (from Jack Bean, Seikagaku, Tokyo, Japan) at 37°C, overnight (to remove terminal N-acetyl glucosamine to result in the M3N2 glycoform). The samples were affinity purified as described above.

*In vitro* glycosylation of Cri-antibodies. *In vitro* GnT1 modification was performed using 1 mg/ml of the M3N2 glycoform antibody as the substrate, and 25 mU/mg of recombinant human  $\beta$ 1,2-mannosyl-UDP-N-acetylglucosaminosyltransferase in a buffer of 100 mM MES, pH 6.5, 5 mM MnCl<sub>2</sub>, 5 mM UDP-GlcNAc, and 0.02% NaN<sub>3</sub> at 32°C for 24 hr. An aliquot was removed for glycan analysis, and the resulting products were affinity purified as described above.

*In vitro* modification of the bisecting-glycoform was carried out using 1 mg/ml of the M3N2 glycoform antibody as the substrate and 25 mU/mg of  $\beta$ 1,2-recombinant human mannosyl-UDP-N-acetylglucosaminosyltransferase I, 25 mU/mg of  $\beta$ 1,2-recombinant human mannosyl-UDP-N-acetylglucosaminosyltransferase II and 3.5 mU/mg of  $\beta$ 1,4-recombinant mouse mannosyl-UDP-N-acetylglucosaminosyltransferase III in a buffer of 100 mM MES pH 6.5, 10 mM MnCl<sub>2</sub>, 5 mM UDP-GlcNAc, and 0.02% NaN<sub>3</sub> at 32°C for 24 hrs. An aliquot was removed for glycan analysis, and the remaining product was affinity purified as described above.

*In vitro* galactosylation was performed using G0 glycoform antibody or bisecting glycoform antibody by contacting the antibody with 0.6 U/mg recombinant bovine milk  $\beta$ 1,4 galactosyltransferase in a buffer of 50 mM Tris-HCl pH 7.4, 150 mM NaCl, 5 mM UDP-galactose, 5 mM MnCl<sub>2</sub>, at 32°C for 24 hrs. An aliquot was removed for glycan analysis, and the remaining products were affinity purified as described above.

*In vitro* sialylation was carried out using the G2 glycoform antibody (1 mg/mL) by contacting it with 0.1 U/mg ST3Gal3 or 0.1 U/mg ST6Gal1, 5 mM CMP-sialic acid, at 32°C for 24 hr in a buffer of 50 mM Tris pH 7.4, 150 mM NaCl, and 3 mM CMP-SA. An aliquot was removed for glycan analysis, and the remaining products were affinity purified as described above.

#### Glycan Analysis:

**Capillary Electrophoresis with Laser Induced Fluorescence Detection.** Buffer components and nucleotide sugars were removed from an aliquot of the glycoremodeled antibody by dilution and concentration in a Microcon™ YM-30 microconcentrator (Millipore, Bedford, MA). N-linked oligosaccharides were released from the protein by contacting it with PNGase F (Prozyme, San Leandro, CA) using the methodology provided by the manufacturer. In brief, the sample was denatured in the buffer of 50 mM sodium phosphate pH 7.5, 0.1% SDS, and 50 mM β-mercaptoethanol for 10 min at 100°C. TX100 was then added to 0.75% (v/v) as well as 10U PNGaseF/200 µg protein. After 3 hours incubation at 37°C, the protein was ethanol precipitated and the supernatant was dried down. The released free oligosaccharides were then labeled with 8-aminopyrene-1,3,6-trisulfonic acid and analyzed by capillary electrophoresis with a carbohydrate labeling and analysis kit from Beckman-Coulter, Inc. (Fullerton, CA), as indicated by the manufacturer (see also, Ma and Nashabeh, 1999, Anal. Chem. 71:5185-5192).

Capillary electrophoresis (CE) was carried out in an eCAP™ N-CHO coated Capillary (50 µm I.D., length to detector 40 cm; Beckman-Coulter, Inc., Fullerton, CA), using a P/ACE™ MDQ Glycoprotein System (Beckman-Coulter, Inc. Fullerton, CA) with Laser Induced Fluorescence Detector (Beckman-Coulter, Inc. Fullerton, CA). Samples were introduced into the cartridge by 20 psi pressure for 10 sec. and separated under 25 kV with reverse polarity for 20 min. Cartridge temperature was kept at 20°C. The electropherogram was generated by laser-induced fluorescence detection at an excitation wavelength of 488 nm and an emission wavelength of 520 nm.

Carbohydrate standards (Calbiochem®, EMD Biosciences, Inc., San Diego, CA), including M3N2 (N-linked trimannosyl core without core fucose), G0 (N-linked oligosaccharide, asialo, agalacto, biantennary with core fucose), G2 (N-linked oligosaccharide, asialo, biantennary with core fucose), and G2 without fucose, S1-G2 (mono-sialylated, galactosylated biantennary oligosaccharide without core fucose) and S2-G2 (di-sialylated, galactosylated biantennary oligosaccharide without core fucose), (from Glyko, see, ProZyme, San Leandro, CA), M3N2F (N-linked trimannosyl core with core fucose) and NGA2F (N-linked oligosaccharide asialo, agalacto, biantennary with core fucose and with bisecting GlcNAc) were labeled with 1-aminopyrene-3,6,8-trisulfonate (APTS, Beckman-

Coulter, Inc. Fullerton, CA) and used to identify the distribution of glycans released from the antibody.

2-AA HPLC. PNGaseF released glycans were labeled with 2-AA (2-anthranilic acid) according to the method described by Anumula and Dhume with slight modifications (1998, Glycobiology 8:685- 694): Reductively-aminated N-glycans were analyzed using a Shodex Asahipak NH2P-50 4D amino column (4.6 mm x 150 mm) (Showa Denko K.K., Tokyo, Japan). The two solvents used for the separation are A) 2% acetic acid and 1% tetrahydrofuran in acetonitrile and B) 5% acetic acid, 3% triethylamine and 1% tetrahydrofuran in water.

10 To separate neutral 2AA-labeled glycans, the column was eluted isocratically with 70% A for 5 minutes, followed by a linear gradient over a period of 60 minutes going from 70% to 50% B, followed by a steep gradient over a period of 5 minutes going from 50% to 5% B and a final isocratic elution with 5% B for 10 minutes. Eluted peaks were detected using fluorescence detection with an excitation at 230 nm and detection wavelength at 420  
15 nm. In this gradient condition, the G0 glycoform will elute at about 30.5 minutes, the G1 glycoform at about 34.0 minutes and the G2 glycoform at about 37.0 minutes. Under these conditions, the presence of fucose does not change the elution time.

To separate anionic 2AA-labeled glycans, the column was eluted isocratically with 70% A for 2.5 minutes, followed by a linear gradient over a period of 97.5 min going from  
20 70% to 5% A and a final isocratic elution with 5% A for 15 minutes. Eluted peaks were detected using fluorescence detection with excitation at 230 nm and detection at 420 nm. In this gradient, neutral glycans are expected to elute between 18.00 - 29.00 minutes, glycans with one charge elute between 30.00 – 40.00 minutes, glycans with two charges elute between 43.00 – 52.00 minutes, glycans with three charges elute between 54.00 – 63.00  
25 minutes, and glycans with four charges elute between 65.00 – 74.00 minutes.

MALDI analysis of reductively-aminated N-glycans. A small aliquot of the PNGase-released N-glycans that were labeled with 2-anthranilic acid (2AA) were then dialyzed for 45 minutes on a MF-Millipore membrane filter (0.025 µm pore, 47 mm dia.), which was floating on water. The dialyzed aliquot was dried in a Speedvac™ (ThermoSavant, Holbrook, NY),  
30 redissolved in a small amount of water, and mixed with a solution of 2,5-dihydroxybenzoic acid (10 g/L) dissolved in water/acetonitrile (50:50).

The mixture was dried onto a MALDI target and analyzed using an Applied Biosystems DE-Pro mass spectrometer (Applied Biosystems, Inc., Foster City, CA) operated in the linear/negative-ion mode. Oligosaccharide structures were assigned based on the observed mass-to-charge ratio and literature precedence. No attempt was made to fully  
 5 characterize isobaric structures.

SDS-PAGE. To determine the stability of the glycoremodeled antibody, all the samples were analyzed by SDS-PAGE. The final products of the samples were run under non-reducing conditions using 8-16% Tris-glycine gel (Invitrogen, Carlsbad, CA). Bovine serum albumin was run under reducing condition as quantitative standards. The gel was  
 10 stained with GelCode Blue Stain Reagent (Pierce Chemical Co., Rockford, IL) for visualization.

The results of the experiments are now described.

Native glycoforms of Cri expressed in human myeloma cells. Cri-IgG1 antibody  
 15 purified from the serum of a patient having multiple myeloma contains variable glycoforms. Figure 97A-97C shows the HPLC profiles of glycans enzymatically released from Cri-IgG1 antibody. Figure 98A-98C shows the MALDI profiles of glycans enzymatically released from Cri-IgG1 antibody expressed in human myeloma cells. The major forms are under-  
 galactosylated G0, G1, while G2 and sialylated structures are relatively minor (Table 14 and  
 20 Figure 97C). To test the impact of modified glycans on the therapeutic properties of the monoclonal antibody, Cri-IgG1 antibody was modified by performing *in vitro* exoglycosidases trimming and *in vitro* glycosylation remodeling to generate different glycoforms of this antibody.

25 **Table 14.** Relative amount of different glycoforms of human myeloma cell-expressed Cri-IgG1 separated by HPLC was calculated from the areas of individual peaks.

Criantibodies	S1G2	G2	G1	G0
DEAE			45.04	54.96
SPA	6	3.17	48.25	51.75
Fc			51.41	38.83

Initially, optimization of each step in exoglycosidases trimming and glycosylation was performed at small scale (100 µg of each).

Trimannosyl core glycoform of Cri-IgG1 Antibody (M3N2). M3N2 was created by stepwise treatment of glycosidases, including neuraminidase,  $\beta$ 1,4-galactosidase and  $\beta$ 1-2, 3, 4, 6 N-acetylhexosaminidase. To assess the removal of terminal galactose and GlcNAc on the glycoremodeled Cri-IgG1 antibody samples, a quantitative capillary electrophoresis (CE) method was used. The glycans were enzymatically released from the glycoremodeled antibody with PNGase F and were derivatized with 8-aminopyrene-1,3,6-trisulfonic acid (APTS) at the reducing terminus. The resulting products were analyzed by CE with on-column laser-induced fluorescence detection (LIF) (Ma & Nashabeh, 1999, *supra*). Since the separation of the glycans is based on the differences in hydrodynamic size, the APTS labeled glycans migrate in order of increasing size (M3N2 < M3N2F < G0 < G1 < G2).

Figures 99A-99D show the electropherograms indicating the glycans released from glycoremodeled Cri-IgG1 antibody as well as glycan standards derivatized with APTS (Figure 99A). The glycoforms were identified by comparing their electrophoretic mobilities to the standards. The relative amount of each glycan species was calculated from the relative area percentage of each indicated peak, and the results are presented in Table 15. The M3N2F glycoform represents 91% of the glycans of DEAE-Cri, 80% of the glycans of SPA-Cri, and 100% of the glycans of Fc-Cri. Incomplete removal of GlcNAc moiety resulting in the GnT-I-M3N2F glycoform (see, Table 15) was observed in the glycan structures from DEAE-Cri (8.6%) and SPA-Cri (~20%). Glycoform GnT-I-M3N2F is the M3N2F glycoform with one additional GlcNAc, such as would be added by GnT-I.

**Table 15.** The areas of individual peaks from CE profile in Fig. 99 were calculated, and relative amounts of the M3N2F and GnT-I-M3N2F glycoforms were determined.

	M3N2F		GnT-I-M3N2F	
	RT (min.)	%	RT (min.)	%
DEAE	10.133	91.4	10.842	8.6
SPA	10.133	80.01	10.842	19.99
Fc	10.133	100	10.842	0

Degalactosylated glycoform (G0). Cri-IgG1 antibody with G0 glycoforms was obtained by stepwise treatment the native Cri-IgG1 antibody with neuraminidase and  $\beta$ 1,4-galactosidase in for 24 hours for each reaction. The glycans released from the glycoremodeled antibody were analyzed by CE, HPLC and MALDI. Figure 100A shows the CE profile of the released glycans. In all three samples, only one peak was observed which was designated as the G0 glycoform based on comparison with the standards (Fig. 100A and Table 16).

**Table 16.** The relative amount of the G0 glycoform of Cri-IgG1 determined by CE and HPLC.

	CE		HPLC	
	RT (min.)	%	RT (min.)	%
DEAE	11.408	100.0	31.194	100.0
SPA	11.408	100.0	31.194	100.0
Fc	11.408	100.0	31.194	100.0

In addition to the glycan analysis provided by CE, a quantitative HPLC method was also used to determine the percent of the G0 glycoform represented by remodeled glycans of the Cri-IgG1 antibody. The glycan distribution on the glycoremodeled antibody was monitored by enzymatically releasing the glycans with PNGase F and derivatizing the released products with 2-anthranilic acid (2-AA) at the reducing terminus. The derivatized mixture was separated by HPLC on a Shodex Asahipak NH2P-50 4D column with fluorescence detection. Figures 101A-101C show the chromatograms obtained from the released glycans. HPLC results confirmed CE analysis, as only one major peak was found in all three samples. In agreement with CE and HPLC data, MALDI analysis also showed almost complete glycoremodeling to the G0 glycoform (Fig. 102A-102C).

Fully galactosylated G2 glycoform (G2). Cri-IgG antibodies were treated with neuraminidase to yield asialo-glycoforms which were also under galactosylated. These asialoglycoforms were then treated with 0.6 U/ml of bovine  $\beta$ 1,4 galactosyltransferase and a galactose donor molecule to glycoremodel the antibody to have the G2 glycoform.

The extent of terminal galactosylation was determined by glycan analysis. Only one major peak was observed in both CE and HPLC profiles (Figure 103A-103C and Fig. 104A-104C). This peak corresponds to the G2 glycoform in each case. Calculation of the percent total peak area showed almost complete (~90%) conversion to the G2 from the under galactosylated glycoforms of the original samples (see, Table 14). These results are summarized in Table 17. MALDI analysis of the glycans further supported the almost to complete glycoremodeling to the G2 glycoform in all of the samples (Fig. 105A-105C).

**Table 17.** Relative amount of G2 glycoform of remodeled Cri-IgI1 antibody determined by percent total peak area in CE and HPLC analysis.

	CE		HPLC	
	RT (min.)	%	RT (min.)	%
DEAE	12.94	90	31.194	100
SPA	12.94	92	31.194	90
Fc	12.94	84	31.194	89

GnT-I-glycoform (GnT-I-M3N2). The M3N2 glycoform Cri-IgG antibody was glycoremodeled to the GnT-I-M3N2 glycoform by adding one GlcNAc moiety to the molecule. The molecule was contacted with 25 mU GnT-I/mg antibody and an appropriate GlcNAc donor molecule. CE, HPLC and MALDI analysis of released glycans (Figures 106A-106D, Figures 107A-107C and Fig. 108A-108C, respectively) indicated that the original M3N2F glycoform was completely remodeled. However, only 40-60% of the modified structures were the GnT-I-M3N2 glycoform, and about 30% were the G0 glycoform. The presence of the G0 glycoform may be the result of incomplete GlcNAc trimming when making the original M3N2 form.

Bisecting glycoform (NGA2F). The M3N2 glycoform Cri-IgG antibody was glycoremodeled to the NGA2F glycoform by contacting it with a combination the three transferases, GnT-I, GnT-II and GnT-III, and an appropriate N-acetylglucosamine donor molecule. The reaction was completed in 24 hours. To determine the extent to which the bisecting-GlcNAc moiety was added to the glycans, CE analysis was used to determine the glycoforms present on the glycoremodeled antibody.

Figure 109A-109D shows the electropherograms obtained from CE analysis of the glycans released from glycoremodeled Cri-IgG1 antibody. Four peaks appeared after remodeling. A major peak migrated at the same retention time as the NGA2F standard glycoform. The three other minor peaks are likely to be the incompletely remodeled glycans.

5 For comparison, a quantitative HPLC method was also used, where the 2-AA labeled glycans eluted in order of increasing size (Gn1 < G0 < NGA2F). As shown in Figure 110A-110C, similar results were obtained from the CE analysis of the glycans. No M3N2F was found using either the CE or HPLC analysis. NGA2F glycans were the major peaks in both CE and HPLC analysis. The Gn1 and G0 glycans still remaining in the sample likely are the result of

10 incomplete modification. Most of the original M3N2F glycoforms were remodeled by three GlcNAc moieties to the NGA2F glycoform (60~70%), about 15~18% were remodeled by the addition of two GlcNAc moieties to the G0 glycoform, and only small amount (~ 7%) were remodeled by the addition of only one GlcNAc moiety. MALDI-MS analysis of the released glycans (Figure 111A-111C) shows peaks of glycoforms with one, two or three terminal

15 GlcNAc moieties, in agreement with CE and HPLC analysis (Figures 109 and 110). The relative amount of each glycan species was calculated from the relative area percentage of each indicated peak, and is summarized in Table 18.

**Table 18.** Relative amounts of different glycoforms from GnT-I, II, and III remodeled Cri-IgG1, as determined by CE and HPLC.

		% Peak Area			
		Retention (min.)	DEAE	SPA	Fc
CE	Peak 1	10.238	6.39	6.89	7.98
	Peak 2	10.775	15.82	14.29	17.9
	Peak 3	11.325	14.14	8.87	15.69
	Bisec.	11.625	63.65	70.04	58.43
HPLC	Peak 1	21.117	37.4	15.02	14
	Peak 2	26.817	12.9	14.24	10.15
	Peak 3	31.224	14.78	2.11	30.2

Bisec.	32.078	34.93	68.63	45.64
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Galactosylated Bisecting (Gal-NGA2F) glycoforms. NGA2F glycoforms of Cri-IgG1 antibodies were glycoremodeled with bovine  $\beta$ 1,4-galactosyltransferase and an appropriate galactose donor. The terminal galactose moieties were added using 0.6 U/ml of  $\beta$ 1,4 galactosyltransferase. Figure 112A-112D shows the electropherograms obtained using the 2-AA HPLC method. In brief, the glycoforms terminating in GalNAc were almost 100% galactosylated. Comparing Figure 112A to Figure 112B for DEAE Cri-IgG1, and Figure 112C to Figure 112D for Fc Cri-IgG1, the 2-AA HPLC profile of GnT-I, II and III modified glycans (Figures 112A and 112C) is modified by GalT1 so that all of the glycan peaks were shifted to elute later due to the size increase from added galactose moieties (Fig. 112B and 112D). These results were further confirmed by MALDI-MS analysis.

Sialylated (S2G2) glycoforms of Cri-IgG1. The glycoremodeled G2 glycoforms of Cri-IgG1 antibody were further remodeled using both ST3Gal3 and ST6Gal1. Figure 113A-113C shows the HPLC profile of the G2 glycoforms remodeled with ST3Gal3. Most of the G2 glycoforms were converted into S2G2 glycoforms (the G2 glycoform with 2 additional terminal sialic acid moieties; ~70%, see, Table 19), and only small amounts were the S1G2 glycoform (the G2 glycoform with 1 additional terminal sialic acid moiety; <25%, see Table 19). These results were further confirmed in the MALDI analysis shown in Figures 114A-114C. MALDI data also shows that all the G2 glycoforms were sialylated to either S2G2 or S1G2 glycoforms.

**Table 19.** Relative amounts of different glycoforms from ST3Gal3 remodeled Cri-IgG1 as determined by HPLC.

	RT (min.)	DEAE	SPA	Fc
S1G2	36.7	25.6	24.83	23.39
	46.9	4.12	6.83	
S2G2	49.4	58.93	50.68	61.88
	52.19	9.1	7.56	6.07

By comparison, ST6Gal1 remodeling of the G0 glycoform did not reach the level of completion found with ST3Gal3 remodeling. Figure 115A-115D and Figure 116A-116C show the results obtained from CE and HPLC analysis, respectively. No S2G2 glycoforms were seen in any of the glycoremodeled samples. However, all of the G2 glycoforms were converted into S1-G2. Analysis from MALDI-MS also supports these data (Figures 117A-117C).

**Stability of remodeled glycans of Cri-IgG1.** Lastly, the stability of the Cri-IgG1 glycans remodeled by exoglycosidase treatment and glycosylation was investigated. Each glycoremodeled Cri-IgG1 antibody was stored at 4°C, and was checked by SDS-PAGE for degradation at two weeks after remodeling. As shown in Figure 118A-118E, the remodeled DEAE and SPA antibodies both retained a molecular weight of about 150 kDa, indicating little to no degradation, regardless of the kind of glycoremodeling performed. The Fc Cri-IgG1 antibody retained a molecular weight of about 38 kDa, also indicating little to no degradation, regardless of the kind of remodeling performed.

Effector Function Bioassay of Remodeled Cri-IgG1 antibodies. The effector function bioassay was derived from the procedure of Mimura et al. (2000, Molecular Immunology 37:697-706). The IC<sub>50</sub> of the glycoforms of Cri-IgG1 antibody was determined by inhibition of the superoxide response of U937 cells elicited by red blood cells sensitized with native anti-NIP antibody.

Monocytic U937 cells were cultured in the presence of 1000 units/mL interferon gamma for 2 days to induce the differentiation of the cells and their capacity to generate superoxide. The cells were then washed and resuspended at  $2 \times 10^6$  cells/mL in Hanks balanced salt solution without phenol red and containing 20 mM HEPES pH 7.4 and 0.15 mM BSA. The red blood cells were sensitized with anti-NIP (5-iodo-4-hydroxy-3-nitrophenacetyl) antibody, in the absence or presence of the various glycoforms of Cri-IgG1 antibody, with incubation at 37°C for 30 minutes. The cells were then washed three times with PBS and resuspended at  $2.5 \times 10^7$  cells/mL in HBSS-BSA. The U937 cells ( $100 \mu\text{L}$ ,  $2 \times 10^6$  cells/mL) were added to plastic tubes and lucigenin ( $20 \mu\text{L}$ , 2.5 mM) was added to the tubes. The tubes were warmed in a 37°C water bath for 5 minutes. The sensitized red blood

cells (80  $\mu$ l,  $2.5 \times 10^7$  /mL) were then added to the tubes. Superoxide anion production was measured by lucigenin-enhanced chemiluminescence at 37°C over a 30 minute period using a Berthold LV953 luminometer (Berthold Australia Pty Ltd, Bundoora, Australia).

The G0 and M3N2 glycoforms Cri-IgG1 antibody had relative inhibitory values of 92% and 85%, respectively, as compared with the native antibody. However, the native CRI-IgG1 antibody lacked core fucose. Shields et al. (2002, J. Biol. Chem. 277:26733-26740) suggests that the lack of core fucose will improve inhibitory values 10 fold. Based on these results, it is anticipated that inhibitory values of the galactosylated-bisecting-G0 glycoform will be greater than the bisecting-G0 glycoform, which in turn will be much greater than the G2 glycoform, which in turn will be approximately equal to the disialylated-G2 glycoform and the monosialylated-G2 glycoform, which in turn will be greater than the native antibody glycoform, which in turn will be greater than the G0 glycoform, which in turn will be greater than the M3N2 glycoform.

## 15 Complement Receptor-1

### 9. Sialylation and Fucosylation of TP10

This example sets forth the preparation of TP10 with sialyl Lewis X moieties and analysis of enhanced biological activity.

Interrupting blood flow to the brain, even for a short time, can trigger inflammatory events within the cerebral microvasculature that can exacerbate cerebral tissue damage. The tissue damage that accrues is amplified by activation of both inflammation and coagulation cascades. In a murine model of stroke, increased expression of P-selectin and ICAM-1 promotes leukocyte recruitment. sCR1 is recombinant form of the extracellular domain of Complement Receptor-1 (CR-1). sCR-1 is a potent inhibitor of complement activation. sCR1sLe<sup>X</sup> (CD20) is an alternately glycosylated form of sCR1 that is alternately glycosylated to display sialylated Lewis<sup>X</sup> antigen. Previously, sCR-1sLe<sup>X</sup> that was expressed and glycosylated *in vivo* in engineered Lec11 CHO cells was found to correctly localize to ischemic cerebral microvessels and C1q-expressing neurons, thus inhibiting neutrophil and platelet accumulation and reducing cerebral infarct volumes (Huang et al., 1999, Science 285:595-599). In the present example, sCR1sLe<sup>X</sup> which was prepared *in vitro*

by remodeling of glycans, exhibited enhanced biological activity similar to that of sCRsLe<sup>x</sup> glycosylated *in vivo*.

The TP10 peptide was expressed in DUK B11 CHO cells. This CHO cell line produces the TP10 peptide with the typical CHO cell glycosylation, with many but not all glycans capped with sialic acid.

**Sialylation of 66 mg of TP10.** TP10 (2.5 mg/mL), CMPSA (5 mM), and ST3Gal3 (0.1 U/mL) were incubated at 32°C in 50 mM Tris, 0.15M NaCl, 0.05% sodium azide, pH 7.2 for 48 hours. Radiolabelled CMP sialic acid was added to a small aliquot to monitor incorporation. TP10 was separated from nucleotide sugar by SEC HPLC. Samples analyzed at 24 hours and 48 hours demonstrated that the reaction was completed after 24 hours. The reaction mixture was then frozen. The reaction products were subjected to Fluorophore Assisted Carbohydrate Electrophoresis (FACE®; Glyko, Inc, Novato CA) analysis (Figure 119).

**Pharmacokinetic studies.** Rats were purchased with a jugular vein cannula. 10 mg/kg of either the pre-sialylation or post-sialylation TP10 peptide was given by tail vein injection to three rats for each treatment (n=3). Fourteen blood samples were taken from 0 to 50 hours. The concentration in the blood of post-sialylation TP10 peptide was higher than that of pre-sialylation TP10 at every time point past 0 hour (Figure 120). Sialic acid addition doubled the area under the plasma concentration-time curve (AUC) of the pharmacokinetic curve as compared to the starting material (Figure 121).

**Fucosylation of sialylated TP10.** 10 mL (25 mg TP10) of the above sialylation mix was thawed, and GDP-fucose was added to 5 mM, MnCl<sub>2</sub> to 5 mM, and FTVI (fucosyltransferase VI) to 0.05 U/mL. The reaction was incubated at 32°C for 48 hours. The reaction products were subjected to Fluorophore Assisted Carbohydrate Electrophoresis (FACE®; Glyko, Inc, Novato CA) analysis (Figure 122). To a small aliquot, radiolabelled GDP-fucose was added to monitor incorporation. TP10 was separated from nucleotide sugar by SEC HPLC. Samples analyzed at 24 hours and 48 hours demonstrated that the reaction was completed at 24 hours. An *in vitro* assay measuring binding to E-selectin indicate that fucose addition can produce a biologically-active E-selectin ligand (Figure 123).

Enbrel™10. GlycoPEGylation of an antibody Enbrel™

This example sets forth the procedures to PEGylate the O-linked glycans of an antibody molecule. Here, Enbrel™ is used as an example, however one of skill in the art will appreciate that this procedure can be used with many antibody molecules.

**Preparation of Enbrel™-SA-PEG (10 kDa).** Enbrel™ (TNF-receptor-IgG<sub>1</sub>-chimera), either with the O-linked glycans sialylated prior to PEGylation or not, is dissolved at 2.5 mg/mL in 50 mM Tris-HCl, 0.15 M NaCl, 5 mM MnCl<sub>2</sub>, 0.05% NaN<sub>3</sub>, pH 7.2. The solution is incubated with 5 mM UDP-galactose and 0.1 U/mL of galactosyltransferase at 32°C for 2 days to cap the undergalactosylated glycans with galactose. To monitor the incorporation of galactose, a small aliquot of the reaction has <sup>14</sup>C-galactose-UDP ligand added; the label incorporated into the peptide is separated from the free label by gel filtration on a Toso Haas G2000SW analytical column in methanol and water. The radioactive label incorporation into the peptide is quantitated using an in-line radiation detector.

When the reaction is complete, the solution is incubated with 1 mM CMP-sialic acid-linker-PEG (10 kDa) and 0.1 U/mL of ST3Gal3 at 32°C for 2 days. To monitor the incorporation of sialic acid-linker-PEG, the peptide is separated by gel filtration on a Toso Haas G3000SW analytical column using PBS buffer (pH 7.1). When the reaction is complete, the reaction mixture is purified using a Toso Haas TSK-Gel-3000 preparative column using PBS buffer (pH 7.1) and collecting fractions based on UV absorption. The fractions containing product are combined, concentrated, buffer exchanged and then freeze-dried. The product of the reaction is analyzed using SDS-PAGE and IEF analysis according to the procedures and reagents supplied by Invitrogen. Samples are dialyzed against water and analyzed by MALDI-TOF MS.

Erythropoietin (EPO)11. Addition of GlcNAc to EPO

This example sets forth the addition of a GlcNAc residue on to a tri-mannosyl core.

**Addition of GlcNAc to EPO.** EPO was expressed in SF-9 insect cells and purified (Protein Sciences, Meriden, CT). A 100% conversion from the tri-mannosyl glycoform of

Epo to the "tri-mannosyl core + 2 GlcNAc" (Peak 1, P1 in Figure 124) was achieved in 24 hours of incubation at 32°C with 100mU/ml of GlcNAcT-I and 100mU/ml of GlcNAcT-II in the following reaction final concentrations:

100mM MES pH 6.5, or 100mM Tris pH 7.5  
 5mM UDP-GlcNAc  
 20mM MnCl<sub>2</sub>  
 100mU/ml GlcNAcT-I  
 100mU/ml GlcNAcT-II  
 1 mg/ml EPO (purified, expressed in Sf9 cells,  
 purchased from Protein Sciences).

**Analysis of glycoforms.** This assay is a slight modification on K-R Anumula and ST Dhume, *Glycobiology* 8 (1998) 685-69. N-glycanase (PNGase) released N-glycans were reductively labeled with anthranilic acid. The reductively-aminated N-glycans were injected onto a Shodex Asahipak NH2P-50 4D amino column (4.6 mm x 150 mm). Two solvents were used for the separation: A) 5% (v/v) acetic acid, 1% tetrahydrofuran, and 3% triethylamine in water, and B) 2% acetic acid and 1% tetrahydrofuran in acetonitrile. The column was then eluted isocratically with 70% B for 2.5 minutes, followed by a linear gradient over a period of 97.5 minutes going from 70 to 5% B and a final isocratic elution with 5% B for 15 minutes. Eluted peaks were detected using fluorescence detection with an excitation of 230 nm and emission wavelength of 420 nm.

Under these conditions, the trimannosyl core had a retention time of 22.3 minutes, and the product of the GnT reaction has a retention time of 30 minutes. The starting material was exclusively trimannosyl core with core GlcNAc (Figure 124).

## 12. Preparation of EPO with multi-antennary complex glycans

This example sets forth the preparation of PEGylated, biantennary EPO, and triantennary, sialylated EPO from insect cell expressed EPO.

Recombinant human erythropoietin (rhEPO) from the baculovirus/Sf9 expression system (Protein Sciences Corp., Meriden, CT) was subjected to glycan analysis and the resulting glycans were shown to be primarily trimannosyl core with core fucose, with a small percentage of glycans also having a single GlcNAc.

**Addition of N-acetylglucosamine with GnT-I and GnT-II.** Two lots of rhEPO (1 mg/mL) were incubated with GnT-I and GnT-II, 5 mM UDP-glcNAc, 20 mM MnCl<sub>2</sub>, and 0.02% sodium azide in 100 mM MES pH 6.5 at 32°C for 24hr. Lot A contained 20 mg of EPO, and 100 mU/mL GnT-I and 60 mU/mL GnT-II. Lot B contained 41 mg of EPO, and 41 mU/mL GnT-I + 50 mU/mL GnT-II. After the reaction, the sample was desalted by gel filtration (PD10 columns, Pharmacia LKB Biotechnology Inc., Piscataway, NJ).

**EPO glycans analyzed by 2-AA HPLC profiling.** This assay is a slight modification on Anumula and Dhume, *Glycobiology* 8 (1998) 685-69. Reductively-aminated N-glycans were injected onto a Shodex Asahipak NH2P-50 4D amino column (4.6 mm x 150 mm). Two solvents were used for the separation, A) 5% (v/v) acetic acid, 1% tetrahydrofuran, and 3% triethylamine in water and B) 2% acetic acid and 1% tetrahydrofuran in acetonitrile. The column was then eluted isocratically with 70% B for 2.5 min, followed by a linear gradient over a period of 100 min going from 70 to 5% B, and a final isocratic elution with 5% B for 20 min. Eluted peaks were detected using fluorescence detection with an excitation of 230 nm and emission wavelength of 420 nm. Non-sialylated N-linked glycans fall in the LC range of 23-34 min, monosialylated from 34-42 min, disialylated from 42-52 min, trisialylated from 55-65 min and tetrasialylated from 68 – 78 min.

Glycan profiling by 2AA HPLC revealed that lot A was 92% converted to a biantennary structure with two GlcNAcs (the balance having a single GlcNAc. Lot B showed 97% conversion to the desired product (Figure 125A and 125B ).

**Introducing a third antennary branch with GnT-V.** EPO (1 mg/mL of lot B) from the product of the GnT-I and GnT-II reactions, after desalting on PD-10 columns and subsequent concentration, was incubated with 10 mU/mL GnT-V and 5 mM UDP-GlcNAc in 100 mM MES pH 6.5 containing 5 mM MnCl<sub>2</sub> and 0.02% sodium azide at 32°C for 24 hrs. 2AA HPLC analysis demonstrated that the conversion occurred with 92% efficiency (Figure 126).

After desalting (PD-10) and concentration, galactose was added with rGalTI: EPO (1 mg/mL) was incubated with 0.1 U/mL GalT1, 5 mM UDP-galactose, 5 mM MnCl<sub>2</sub> at 32°C for 24 hrs.

**MALDI analysis of reductively-aminated N-glycans from EPO.** A small aliquot of the PNGase released N-glycans from EPO that had been reductively labeled with

anthranilic acid was dialyzed for 45 min on an MF-Millipore membrane filter (0.025  $\mu$ m pore, 47 mm dia), which was floating on water. The dialyzed aliquot was dried in a speedvac, redissolved in a small amount of water, and mixed with a solution of 2,5-dihydroxybenzoic acid (10 g/L) dissolved in water/acetonitrile (50:50). The mixture was  
5 dried onto the target and analyzed using an Applied Biosystems DE-Pro MALDI-TOF mass spectrometer operated in the linear/negative-ion mode. Oligosaccharides were assigned based on the observed mass-to-charge ratio and literature precedence.

Analysis of released glycans by MALDI showed that galactose was added quantitatively to all available sites (Figure 127). Galactosylated EPO from above was then  
10 purified by gel filtration on a Superdex 1.6/60 column in 50 mM Tris, 0.15M NaCl, pH 6.

**Sialylation.** After concentration and desalting (PD-10), 10 mg galactosylated EPO (1 mg/mL) was incubated with ST3Gal3 (0.05 U/mL), and CMP-SA (3 mM) in 50 mM Tris, 150 mM NaCl, pH 7.2 containing 0.02% sodium azide. A separate aliquot contained radiolabelled CMP-SA. The resulting incorporated label and free label was separated by  
15 isocratic size exclusion chromatography/HPLC at 0.5mL/min in 45% MeOH, 0.1%TFA (7.8mm x 30 cm column, particle size 5  $\mu$ m, TSK G2000SW<sub>XL</sub>, Toso Haas, Ansys Technologies, Lake Forest, CA). Using this procedure, 12% of the counts were incorporated (360 micromolar, at 33 micromolar EPO, or about 10.9 moles/mole). Theoretical (3 N-linked sites, tri-antennary) is about 9 moles/mole incorporation. These correspond within the limits  
20 of the method. In an identical reaction with ST6Gal1 instead of ST3Gal3, 5.7% of the radiolabel was incorporated into the galactosylated EPO, or about 48% compared with ST3Gal3.

### 13. GlycoPEGylation of EPO produced in insect cells

25 This example sets forth the preparation of PEGylated biantennary EPO from insect cell expressed EPO.

Recombinant human erythropoietin (rhEPO) from the baculovirus/Sf9 expression system (Protein Sciences Corp., Meriden, CT) was subjected to glycan analysis and the resulting glycans were shown to be primarily trimannosyl core with core fucose, with a small  
30 percentage of glycans also having a single GlcNAc (Figure 128).

**Addition of N-acetylglucosamine with GnT-I and GnT-II.** Two lots of rhEPO (1 mg/mL) were incubated with GnT-I and GnT-II, 5 mM UDP-glcNAc, 20 mM MnCl<sub>2</sub>, and 0.02% sodium azide in 100 mM MES pH 6.5 at 32°C for 24hr. Lot A contained 20 mg of EPO, and 100 mU/mL GnT-I and 60 mU/mL GnT-II. Lot B contained 41 mg of EPO, and 41 mU/mL GnT-I + 50 mU/mL GnT-II. After the reaction, the sample was desalted by gel filtration (PD10 columns, Pharmacia LKB Biotechnology Inc., Piscataway, NJ).

Glycan profiling by 2AA HPLC revealed that lot A was 92% converted to a biantennary structure with two GlcNAcs (the balance having a single glcNAc. Lot B showed 97% conversion to the desired product (Figure 125A and 125B ).

**Galactosylation of EPO lot A.** EPO (~16 mgs of lot A) was treated with GnT-II to complete the addition of GlcNAc. The reaction was carried out in 50 mM Tris pH 7.2 containing 150 mM NaCl, EPO mg/ml, 1 mM UDP-GlcNAc, 5 mM MnCl<sub>2</sub>, 0.02% sodium azide and 0.02 U/ml GnT-II at 32 °C for 4 hrs. Then galactosylation of EPO was done by adding UDP-galactose to 3 mM and GalT1 to 0.5 U/ml and the incubation continued at 32° C for 48 hrs.

Galactosylated EPO was then purified by gel filtration on a Superdex75 1.6/60 column in 50 mM Tris, 0.15M NaCl, pH 6. The EPO containing peak was then analyzed by 2AA HPLC. Based on the HPLC data ~85% of the glycans contains two galactose and ~15% of the glycans did not have any galactose after galactosylation reaction.

**Sialylation of galactosylated EPO.** Sialylation of galactosylated EPO was carried out in 100 mM Tris pH containing 150 mM NaCl, 0.5 mg/ml EPO, 200 mU/ml of ST3Gal3 and either 0.5 mM CMP-SA or CMP-SA-PEG (1 kDa) or CMP-SA-PEG (10 kDa) for 48 hrs at 32 °C. Almost all of the glycans that have two galactose residues were fully sialylated (2 sialic acids / glycan) after sialylation reaction with CMP-SA. MALDI-TOF analysis confirmed the HPLC data.

**PEGylation of galactosylated EPO.** For PEGylation reactions using CMP-SA-PEG (1 kDa) and CMP-SA-PEG (10 kDa), an aliquot of the reaction mixture was analyzed by SDS-PAGE (Figure 129). The molecular weight of the EPO peptide increased with the addition of each sugar, and increased more dramatically in molecular weight after the PEGylation reactions.

***In vitro* bioassay of EPO.** *In vitro* EPO bioassay (adapted from Hammerling et al, 1996, J. Pharm. Biomed. Anal. 14: 1455-1469) is based on the responsiveness of the TF-1 cell line to multiple levels of EPO. TF-1 cells provide a good system for investigating the proliferation and differentiation of myeloid progenitor cells. This cell line was established by  
5 T. Kitamura et al. in October 1987 from a heparinized bone marrow aspiration sample from a 35 year old Japanese male with severe pancytopenia. These cells are completely dependent on Interleukin 3 or Granulocyte-macrophage colony-stimulating factor (GM-CSF).

The TF-1 cell line (ATCC, Cat. No. CRL-2003) was grown in RPMI + FBS 10% + GM-CSF (12 ng/ml) and incubated at 37°C 5% CO<sub>2</sub>. The cells were in suspension at a  
10 concentration of 5000 cells/ml of media, and 200 µl were dispensed in a 96 well plate. The cells were incubated with various concentrations of EPO (0.1 µg/ml to 10 µg/ml) for 48 hours. A MTT Viability Assay was then done by adding 25 µl of MTT at 5 mg/ml (SIGMA M5655), incubating the plate at 37°C for 20 min to 4 hours, adding 100 µl of isopropanol/HCl solution (100 ml isopropanol + 333 µl HCl 6N), reading the OD at 570 nm,  
15 and 630nm or 690nm, and subtracting the readings at 630 nm or 690 nm from the readings at 570 nm.

Figure 130 contains the results when sialylated EPO, and EPO glycoPEGylated with 1 kDa or 10 kDa PEG was subjected to an *in vitro* EPO bioactivity test. The EPO glycoPEGylated with 1kDa PEG had almost the same activity as the unglycoPEGylated EPO  
20 when both were at a concentration of approximately 5 µg/ml. The EPO glycoPEGylated with 10 kDa PEG had approximately half the activity of the unglycoPEGylated EPO when both were at a concentration of approximately 5 µg/ml.

#### 14. GlycoPEGylation of O-Linked Glycans of EPO produced in CHO Cells

**Preparation of O-linked EPO-SA-PEG (10 kDa).** Asialo-EPO, originally produced  
25 in CHO cells, is dissolved at 2.5 mg/mL in 50 mM Tris-HCl, 0.15 M NaCl, 0.05% NaN<sub>3</sub>, pH 7.2. The solution is incubated with 5 mM CMP-SA and 0.1 U/mL of ST3Gal3 at 32°C for 2 days. To monitor the incorporation of sialic acid onto the N-linked glycans, a small aliquot of the reaction had CMP-SA-<sup>14</sup>C added; the peptide is separated by gel filtration on a Toso  
30 Haas G2000SW analytical column using methanol, water and the product detected using a

radiation detector. When the reaction is complete, the solution is concentrated using a Centricon-20 filter. The remaining solution is buffer exchanged with 0.05 M Tris (pH 7.2), 0.15 M NaCl, 0.05% NaN<sub>3</sub> to a final volume of 7.2 mL until the CMP-SA could no longer be detected. The retentate is then resuspended in 0.05 M Tris (pH 7.2), 0.15 M NaCl, 0.05% NaN<sub>3</sub> at 2.5 mg/mL protein. The solution is incubated with 1 mM CMP-SA-PEG (10 kDa) and ST3Gal1, to glycosylate the O-linked site, at 32°C for 2 days. To monitor the incorporation of sialic acid-PEG, a small aliquot of the reaction is separated by gel filtration using a Toso Haas TSK-gel-3000 analytical column eluting with PBS pH 7.0 and analyzing by UV detection. When the reaction is complete, the reaction mixture is purified using a Toso Haas TSK-gel-3000 preparative column using PBS buffer (pH 7.0) collecting fractions based on UV absorption. The product of the reaction is analyzed using SDS-PAGE and IEF analysis according to the procedures and reagents supplied by Invitrogen. Samples are dialyzed against water and analyzed by MALDI-TOF MS.

#### 15                    15. EPO-Transferrin

This example sets forth the procedures for the glycoconjugation of proteins to O-linked glycans, and in particular, transferrin is glycoconjugated to EPO. The sialic acid residue is removed from O-linked glycan of EPO, and EPO-SA-linker-SA-CMP is prepared. EPO-SA-linker-SA-CMP is glycoconjugated to asialotransferrin with ST3Gal3.

20                    **Preparation of O-linked asialo-EPO.** EPO (erythropoietin) produced in CHO cells is dissolved at 2.5 mg/mL in 50 mM Tris 50 mM Tris-HCl pH 7.4, 0.15 M NaCl, and is incubated with 300 mU/mL sialidase (*Vibrio cholera*)-agarose conjugate for 16 hours at 32 °C. To monitor the reaction a small aliquot of the reaction is diluted with the appropriate buffer and a IEF gel performed according to Invitrogen procedures. The mixture is  
25                    centrifuged at 10,000 rpm and the supernatant is collected. The supernatant is concentrated to a EPO concentration of about 2.5 mg/mL in 50 mM Tris-HCl, 0.15 M NaCl, 0.05% NaN<sub>3</sub>, pH 7.2. The solution is incubated with 5 mM CMP-sialic acid and 0.1 U/mL of ST3Gal3 at 32°C for 2 days. To monitor the incorporation of sialic acid, a small aliquot of the reaction had CMP-SA-fluorescent ligand added; the label incorporated into the peptide is separated  
30                    from the free label by gel filtration on a Toso Haas G3000SW analytical column using PBS buffer (pH 7.1). When the reaction is complete, the reaction mixture is purified using a Toso

Haas G3000SW preparative column using PBS buffer (pH 7.1) and collecting fractions based on UV absorption. The product of the reaction is analyzed using SDS-PAGE and IEF analysis according to the procedures and reagents supplied by Invitrogen. Samples are dialyzed against water and analyzed by MALDI-TOF MS.

5           **Preparation of EPO-SA-linker-SA-CMP.** The O-linked asialo-EPO 2.5 mg/mL in 50 mM Tris-HCl, 0.15 M NaCl, 0.05% NaN<sub>3</sub>, pH 7.2. The solution is incubated with 1 mM CMP-sialic acid-linker-SA-CMP and 0.1 U/mL of ST3Gal1 at 32°C for 2 days. To monitor the incorporation of sialic acid-linker-SA-CMP, the peptide is separated by gel filtration on a Toso Haas G3000SW analytical column using PBS buffer (pH 7.1).

10           After 2 days, the reaction mixture is purified using a Toso Haas G3000SW preparative column using PBS buffer (pH 7.1) and collecting fractions based on UV absorption. The product of the reaction is analyzed using SDS-PAGE and IEF analysis according to the procedures and reagents supplied by Invitrogen. Samples are dialyzed against water and analyzed by MALDI-TOF MS.

15           **Preparation of Transferrin-SA-Linker-SA-EPO.** EPO-SA-Linker-SA-CMP from above is dissolved at 2.5 mg/mL in 50 mM Tris-HCl, 0.15 M NaCl, 0.05% NaN<sub>3</sub>, pH 7.2. The solution is incubated with 2.5 mg/mL asialo-transferrin and 0.1 U/mL of ST3Gal3 at 32°C for 2 days. To monitor the incorporation of transferrin, the peptide is separated by gel filtration on a Toso Haas G3000SW analytical column using PBS buffer (pH 7.1) and the  
20           product detected by UV absorption. When the reaction is complete, the solution is incubated with 5 mM CMP-SA and 0.1 U/mL of ST3Gal3 (to cap any unreacted transferrin glycans) at 32°C for 2 days. The reaction mixture is purified using a Toso Haas G3000SW preparative column using PBS buffer (pH 7.1) collecting fractions based on UV absorption. The product of the reaction is analyzed using SDS-PAGE and IEF analysis according to the procedures  
25           and reagents supplied by Invitrogen. Samples are dialyzed against water and analyzed by MALDI-TOF MS.

#### 16. EPO-GDNF

30           This example sets forth the procedures for the glycoconjugation of proteins, and in particular, the preparation of EPO-SA-Linker-SA-GDNF.

**Preparation of EPO-SA-Linker-SA-GDNF.** EPO-SA-Linker-SA-CMP from above is dissolved at 2.5 mg/mL in 50 mM Tris-HCl, 0.15 M NaCl, 0.05% NaN<sub>3</sub>, pH 7.2. The solution is incubated with 2.5 mg/mL GDNF (produced in NSO) and 0.1 U/mL of ST3Gal3 at 32°C for 2 days. To monitor the incorporation of GDNF, the peptide is separated by gel  
5 filtration on a Toso Haas G3000SW analytical column using PBS buffer (pH 7.1) and the product detected by UV absorption. When the reaction is complete, the solution is incubated with 5 mM CMP-SA and 0.1 U/mL of ST3Gal3 (to cap any unreacted GDNF glycans) at 32°C for 2 days. The reaction mixture is purified using a Toso Haas G3000SW preparative column using PBS buffer (pH 7.1) collecting fractions based on UV absorption. The product  
10 of the reaction is analyzed using SDS-PAGE and IEF analysis according to the procedures and reagents supplied by Invitrogen. Samples are dialyzed against water and analyzed by MALDI-TOF MS.

#### 17. Mono-antennary GlycoPEGylation of EPO

15 This example sets forth the procedure for the preparation of glycoPEGylated mono-antennary erythropoietin (EPO), and its bioactivity *in vitro* and *in vivo*.

When EPO (GenBank Accession No. P01588) is expressed in CHO cells, N-linked glycans are formed at amino acid residues 24, 38 and 83, and an O-linked glycan is formed at amino acid residue 126 (Fig. 131; Lai et al., 1986, J. Biol. Chem. 261:3116-3121). The  
20 bioactivity of this glycoprotein is directly correlated with the level of NeuAc content. Increased sialic acid decreases the binding of EPO to its receptor *in vitro*; however increased sialic acid increases the bioactivity of EPO *in vivo*. The O-linked glycan has no impact on the *in vitro* or *in vivo* activity of EPO, or the pharmacokinetics of the molecule (Wasley et al., 1991, Blood 77:2624-2632).

25 When EPO is expressed in insect cells, such as is accomplished using a baculovirus/Sf9 expression system (see also, Wojchowshi et al., 1987, Biochem. Biophys. Acta 910:224-232; Quelle et al., 1989, Blood 74:652-657), N-linked glycans are formed at amino acid residues 24, 38 and 83, but an O-linked glycan is not formed at amino acid residue 126 (Fig. 132). This is because the insect cell does not have a glycosyl transferase  
30 that recognizes the amino acid sequence around amino acid residue 126 of EPO. The majority of the N-linked glycans are composed of GlcNAc<sub>2</sub>Man<sub>3</sub>Fuc. In the present example,

EPO expressed in insect cells was remodeled with high efficiency to achieve the complex glycan SA<sub>2</sub>Gal<sub>2</sub>GlcNAc<sub>2</sub>Man<sub>3</sub>FucGlcNAc<sub>2</sub> by contacting the protein with, in series, GnT1,2, GalT-1, and ST in the presence of the appropriate donor molecules. These enzymatic reactions were performed on insect cell expressed EPO using reaction conditions disclosed herein, to yield the complex glycans herein with 92% total efficiency (Table 21). Optionally, O-linked glycans can also be added (O'Connell and Tabak, 1993, J. Dent. Res. 72:1554-1558; Wang et al., 1993, J. Biol. Chem. 268:22979-22983).

**Table 21.** Percent of each species of glycan structure in the population of glycan structures on insect cell expressed EPO ("starting material"), and on EPO after each sequential enzymatic remodeling step.

sequential enzymatic remodeling step.				
Glycan	Starting Material	After GnT-I, II	After GalT-I	After ST
	0.5%			
	98.0%			
	1.0%	0.5%	0.5%	
	0.5%	99.5%	4%	2%

EPO having monoantennary PEGylated glycan structures is prepared by expressing EPO peptide in insect cells, then contacting the EPO peptide with GnTI only (or alternatively GnTII only) in the presence of a GlcNAc donor. The EPO peptide is then contacted with GalT-I in the presence of a galactose donor. The EPO peptide is then contacted with ST in the presence of SA-PEG donor molecules (Fig. 134A) to generate an EPO peptide having three N-linked mono-antennary PEGylated glycan structures (Fig. 134B).

The *in vitro* bioactivity of EPO-SA and EPO-SA-PEG generated from insect cell expressed EPO was accessed by measuring the ability of the molecule to stimulate the proliferation of TF-1 erythroleukemia cells. Tri-antennary EPO-SA-PEG 1 kDa exhibited almost all of the bioactivity of tri-antennary EPO-SA, and di-antennary EPO-SA-PEG 10 kDa exhibited almost all of the bioactivity of di-antennary EPO-SA over a range of EPO concentrations (Fig. 135). Remodeled and glycoPEGylated EPO generated in insect cells exhibited up to 94% of the *in vitro* bioactivity of Epogen™, which is EPO expressed in CHO cells without further glycan remodeling or PEGylation (Table 22).

**Table 22.** *In vitro* activity of the EPO constructs as compared with Epogen™ at 2 µg/ml protein and 48 hr.

Compound (2 µg/ml protein)	Activity ( percent of Epogen™)
Biantennary-SA	146
Biantennary-SA-PEG 1K	94
Biantennary-SA-PEG 10K	75
Triantennary-SA 2,3 <sup>1</sup>	42
Triantennary-SA-PEG 1K	48
Triantennary-SA-PEG 10K	34

<sup>1</sup> The triantennary –SA 2,3 construct has the SA molecule bonded in a 2,3 linkage.

The *in vivo* pharmacokinetics of glycoPEGylated and non-glycoPEGylated EPO was determined. GlycoPEGylated and non-glycoPEGylated [<sup>125</sup>I]-labeled EPO was bolus injected into rats and the pharmacokinetics of the molecules were determined. As compared with bi-antennary EPO, the AUC of bi-antennary EPO-PEG 1 kDa was 1.8 times greater, and the AUC of bi-antennary EPO-PEG 10 kDa was 11 times greater (Fig. 136). As compared with

bi-antennary EPO, the AUC of bi-antennary EPO-PEG 1 kDa was 1.6 times greater, and the AUC of bi-antennary EPO-PEG 10 kDa was 46 times greater (Fig. 136). Therefore, the pharmacokinetics of EPO was greatly improved by glycoPEGylation.

The *in vivo* bioactivity of glycoPEGylated and non-glycoPEGylated EPO was also determined by measuring the degree to which the EPO construct could stimulate reticulocytosis. Reticulocytosis is a measure of the rate of the maturation of red blood cell precursor cells into mature red blood cells (erythrocyte). Eight mice per treatment group were given a single subcutaneous injection of 10 µg protein/Kg, and the percent reticulocytes was measured at 96 hours (Fig. 137). Tri- and bi-antennary PEGylated EPO exhibited greater *in vivo* bioactivity than non-PEGylated EPO forms, including Epogen™.

Further determination of *in vivo* bioactivity of the EPO constructs was assessed by measuring the hematocrit (the percent of whole blood that is comprised of red blood cells) of CD-1 female mice 15 days after intraperitoneal injection three times per week with 2.5 µg peptide/kg body weight of the EPO construct. The hematocrit increment increased with the size of the EPO form, with the 82.7 kDa mono-antennary EPO-PEG 20 kDa having a slightly greater activity than the 35.6 kDa NESP (Aranesp™) and about two times the bioactivity of 28.5 kDa Epogen™ (Fig. 138).

This example illustrates that the generation of a longer-acting glycoPEGylated EPO is feasible. The pharmacokinetic profile of glycoPEGylated EPO can be customized by altering the number of glycoPEGylation sites and the size of the PEG molecule added to alter the half-life of the peptide in the bloodstream. Finally, glycoPEGylated EPO retains both *in vitro* and *in vivo* bioactivity.

#### 18. Preparation and Bioactivity of Sialylated and PEGylated Mono-, Bi- and Tri-Antennary EPO

This example illustrates the production of glycoPEGylated EPO, in particular PEGylated EPO having mono-antennary and bi-antennary glycans with PEG linked thereto. The following EPO variants were produced: mono-antennary PEG (1 kDa), PEG (10 kDa) and PEG (20 kDa); bi-antennary 2,3-sialic acid (SA), bi-antennary SA-PEG (1 kDa), bi-antennary SA-PEG (10 kDa); tri-antennary 2,3-SA and tri-antennary 2,6-SA capped with 2,3-SA.

Recombinant erythropoietin (rEPO) expressed in insect cells was obtained from Protein Sciences (Lot # 060302, Meridan CT). The glycan composition of this batch of EPO had approximately 98% trimannosyl core structure. Figure 139A depicts the HPLC analysis of the released glycans from this EPO, with peak "P2" representing the trimannosyl core glycan. Figure 139B shows the MALDI analysis of the released glycans with the structures of the released glycans beside the peak they represent.

#### **Mono-antennary branching**

Several steps were performed to produce the mono-antennary branched structure. In brief, the first step was a GnT-I/GalT-1 reaction followed by purification using Superdex-75 chromatography. This reaction adds a GlcNAc moiety to one branch of the tri-mannosyl core, and a galactose moiety onto the GlcNAc moiety. Branching was extended with the ST3Gal3 reaction to add the SA-PEG (10 kDa) moiety or the SA-PEG (20 kDa) moiety onto the terminal galactose moiety. The final purification was accomplished using Superdex-200 chromatography (Amersham Biosciences, Arlington Heights, IL).

**GnT-I/GalT-1 Reaction.** The GnT-I and GalT-1 reactions were combined and incubated at 32°C for 36 hours. The reaction contained 1 mg/mL EPO, 100 mM Tris-Cl pH 7.2, 150 mM NaCl, 5 mM MnCl<sub>2</sub>, 0.02% NaN<sub>3</sub>, 3 mM UDP-GlcNAc, 50 mU/mg GnT-I, 3 mM UDP-Gal, and 200 mU/mg GalT-1. Figure 140 depicts the MALDI analysis of glycans released from EPO after the GnT-I/GalT-1 reaction. Glycan analysis showed approximately 90% of the glycans had the desired mono-antennary branched structure with a terminal galactose moiety.

**Superdex 75 Purification.** After the GnT-I/GalT1 reaction, EPO was purified from the enzyme protein contaminants and nucleotide sugars using a 1.6 cm x 60 cm Superdex-75 gel filtration chromatography (Amersham Biosciences, Arlington Heights, IL) in PBS containing 0.02% Tween 20 (Sigma-Aldrich Corp., St. Louis, MO).

**ST3Gal3 Reaction.** The ST3Gal3 PEGylation reaction was incubated at 32°C for 24 hours. The reaction contained 1 mg/mL EPO, 100 mM Tris-Cl pH 7.2, 150 mM NaCl, 0.02% NaN<sub>3</sub>, 200 mU/mg ST3Gal3, and 0.5 mM CMP-SA-PEG (10 kDa) or 0.5 mM CMP-SA-PEG (20 kDa). Figure 141 depicts the SDS-PAGE analysis of EPO after this reaction. The corresponding molecular weights of the protein bands indicate that the EPO glycans formed by the GnT-I/GalT-1 reaction were completely sialylated with the PEG derivative.

**Superdex 200 Purification.** EPO then was purified from the contaminants of the ST3Gal3 reaction by a 1.6 cm x 60 cm Superdex-200 gel filtration chromatography (Amersham Biosciences, Arlington Heights, IL) in PBS containing 0.02% Tween-20.

**TF-1 Cell *In Vitro* Bioassay of Mono-antennary PEGylated EPO.** The TF-1 cell line is used to assess the activity of EPO *in vitro*. The TF-1 cells line is a myeloid progenitor cell line available from the American Type Culture Collection (Catalogue No. CRL-2003, Rockville, MD). The cell line is completely dependant on Interleukin-3 or Granulocyte-Macrophage Colony-Stimulating Factor for viability. TF-1 cells provide a good system for investigating the effect of EPO on proliferation and differentiation.

The TF-1 cells were grown in RPMI with 10% FBS and 12 ng/ml GM-CSF at 37°C in 5% CO<sub>2</sub>. The cells were suspended at a concentration of 10,000 cells/ml of media. 200 µl aliquots of cells were dispensed into a 96-well plate. The cells were incubated with 0.1 to 10 µg/ml EPO for 48 hrs.

The MTT viability assay was then performed by first adding 25 µl of 5 µg/ml MTT (3-[4,5-dimethylthiazol-2-yl]-2,5-diphenyltetrazolium bromide, or thiazolyl blue; Sigma Chemical Co., St. Louis, Mo., Catalogue No. M5655). The plate was incubated for 4 hrs at 37°C. 100 µl of isopropanol/HCl solution (100 ml isopropanol and 333 µl HCl 6N) was added. The absorbency of the plates was read at 570 nm and either 630 or 690 nm, and the reading at either 630 nm or 690 nm was subtracted for the reading at 570 nm.

Figure 142 depicts the results of the bioassay of EPO activity after PEGylation of it mono-antennary glycans. In this bioassay, the mono-antennary PEGylated EPO is much less active than a non-PEGylated EPO (Epogen).

***In Vivo* Bioassay of Mono-antennary PEGylated EPO – Examination of Hematological Parameters.**

The effect of EPO-SA-PEG (10 kDa) and EPO-SA-PEG (20 kDa), the preparation of which compounds is described in detail above, on hematological parameters of male Sprague Dawley rats was examined. Sprague Dawley rats are a well-studied experimental model and techniques for the use and care of such animals are well-known to those skilled in the art. Therefore, Sprague Dawley rats provide a good system for studying the clinical and

physiological effects of EPO-SA-PEG (10 kDa) and EPO-SA-PEG (20 kDa) according to the present invention.

**Preparation, Care, and Handling of Test Subjects.** *In vivo* testing in accordance with the methods and compositions of the present invention was conducted at TherImmune Research Corporation (Gaithersburg, MD). Test subjects for the *in vivo* studies included 170 male Sprague Dawley rats, obtained from Harlan (Harlan Sprague Dawley, Inc., Indianapolis, IN). Subjects were all at least 300 grams in weight and at least 70 days old at the time of shipment. Subjects were cared for according to TherImmune's Institutional Animal Care and Use Committee, in accordance with provisions of the USDA Animal Welfare Act, the PHS Policy on Humane Care and Use of Laboratory Animals, and the U.S. Interagency Research Animal Committee Principles for the Utilization and Care of Research Animals. The study was conducted in accordance with the FDA Good Laboratory Practice Standards, 21 CFR Part 58. Subjects were housed individually in polycarbonate cages, under controlled environmental conditions, and were provided fresh food weekly, *ad libitum*, and tap water was made available to test subjects *ad libitum* via either an automatic watering system or water bottles.

Subjects were randomly assigned to groups for testing, and the minimum number of animals needed to give biologically meaningful data were used. Subjects were dosed via subcutaneous injection, and dosing frequency and quantity is indicated in in Table 25, and were observed prior to dose administration, and at least twice daily for signs of toxicity, moribundity and mortality. Body weights were measured and physical examinations were conducted on subjects pre- and post-study, as well as on a weekly basis during the study.

For hematology studies, a 0.25 ml ( $\pm$  15%) sample of blood was collected from the jugular vein of all surviving subjects prior to the first dose on study day one, as well as on study days 3, 5, 8, 10, 12, 15, 17, 19, 22, 24, 26 and 29. Hematological analysis of the blood of the test subjects included examination of cellular morphology, erythrocyte count, hematocrit, hemoglobin, leukocyte, leukocyte differential, mean cell hemoglobin, mean cell hemoglobin concentration, mean cell volume, mean platelet volume, platelet count, and reticulocytes.

**Table 25.** Summary of test subject grouping and dosage.

Group	Treatment	Dose (ug/kg)	Dose Volume (ml/kg)	Concentration (ug/ml)	Dose Frequency	Number of Animals
1	Vehicle	-	0.33	-	Every 3 days <sup>1</sup>	10
2	P113	2.5	0.33	7.5	Every 3 days <sup>1</sup>	5
3	P113	6.0	0.33	18	Every 3 days <sup>1</sup>	5
4	P140	2.5	0.33	7.5	Every 3 days <sup>1</sup>	5
5	P140	6.0	0.33	18	Every 3 days <sup>1</sup>	5
6	P138	2.5	0.33	7.5	Every 3 days <sup>1</sup>	5
7	P138	6.0	0.33	18	Every 3 days <sup>1</sup>	5
8	P139	2.5	0.33	7.5	Every 3 days <sup>1</sup>	5
9	P139	6.0	0.33	18	Every 3 days <sup>1</sup>	5
10	Vehicle	-	0.33	-	Every 5 days <sup>2</sup>	10
11	P140	4	0.33	12	Every 5 days <sup>2</sup>	5
12	P140	12	0.33	36	Every 5 days <sup>2</sup>	5
13	P138	4	0.33	12	Every 5 days <sup>2</sup>	5
14	P138	12	0.33	36	Every 5 days <sup>2</sup>	5
15	P139	4	0.33	12	Every 5 days <sup>2</sup>	5
16	P139	12	0.33	36	Every 5 days <sup>2</sup>	5
17	Vehicle	-	0.33	-	Every 7 days <sup>3</sup>	10
18	P140	6	0.33	18	Every 7 days <sup>3</sup>	5
19	P140	25	0.33	75	Every 7 days <sup>3</sup>	5
20	P138	6	0.33	18	Every 7 days <sup>3</sup>	5
21	P138	25	0.33	75	Every 7 days <sup>3</sup>	5
22	P139	6	0.33	18	Every 7 days <sup>3</sup>	5
23	P139	25	0.33	75	Every 7 days <sup>3</sup>	5
24	Vehicle	-	0.33	-	Every 10 days <sup>4</sup>	10
25	P140	7.5	0.33	23	Every 10 days <sup>4</sup>	5
26	P140	50	0.33	150	Every 10 days <sup>4</sup>	5
27	P138	7.5	0.33	23	Every 10 days <sup>4</sup>	5
28	P138	50	0.33	150	Every 10 days <sup>4</sup>	5
29	P139	7.5	0.33	23	Every 10 days <sup>4</sup>	5
30	P139	50	0.33	150	Every 10 days <sup>4</sup>	5

5

Study days are indicated for each group of subjects as follows:

1 = SD 1, 4, 7, 10, 13, 16, 19, 22, 25 and 28

2 = SD 1, 6, 11, 16, 21 and 27

3 = SD 1, 8, 15 and 22

4 = SD 1, 11 and 21

10

On study day 29, after clinical pathology blood collection, all surviving subjects were euthanized via carbon dioxide inhalation. Blood was collected from the abdominal aorta. Moribund subjects that were previously euthanized, as well as subjects found dead during the study, were subjected to full necropsy.

5        **Analysis of results and interpretation of data.** Quantitative results were analyzed using techniques known to those skilled in the relevant art. In particular, results were analyzed using the Kolmogorov-Smirnov test for normality, the Levene Median test for equal variance, and one-way Analysis of Variance (ANOVA). In instances where the normality or equal variance test failed, the analysis was continued using the non-parametric Kruskal-  
10       Wallis ANOVA on rank-transformed data. Parametric data was analyzed using the Dunnett's t-test to delineate which groups differed from the control. For non-parametric data, the Dunns test was used to delineate which groups differed from the control. A probability value of less than 0.05 (two-tailed) was used as the critical level of significance for all tests.

Based on one analysis of the data from the first fifteen days of the study, it was shown  
15       that a single dose of 50 µg/kg of glycoPEGylated monoantennary EPO, either EPO-SA-PEG (10 kDa) or EPO-SA-PEG (20 kDa) according to the present invention, gives an extended rise in blood hemoglobin in rats, comparable to the effect of NESP given at the same dose (Figure 192). Not wishing to be bound by any particular theory, Figure 192 illustrates that EPO-SA-PEG (10 kDa) and EPO-SA-PEG (20 kDa) have unexpectedly enhanced biological  
20       properties.

### **Bi-antennary Branching**

Several reactions were performed to accomplish the bi-antennary branching of EPO. Briefly, the first reaction combined the GnT-I and GnT-II reactions to add GlcNAc moieties  
25       to two of the tri-mannosyl core branches. The second reaction, the GalT-1 reaction, adds a galactose moiety to each GlcNAc moieties. Superdex 75 chromatography (Amersham Biosciences, Arlington Heights, IL) was performed prior to the ST3Gal3 reaction. The bi-antennary branching was further extended with the ST3Gal3 reaction to add either a 2,3-SA, or SA-PEG (1 kDa), SA-PEG (10 kDa). Final purification was accomplished using Superdex  
30       200 chromatography (Amersham Biosciences, Arlington Heights, IL).

**GnT-I/GnT-II Reaction.** The GnT-I and GnT-II reactions were combined and incubated at 32°C for 48 hours. The reaction contained 1 mg/mL EPO, 100 mM MES pH 6.5, 150 mM NaCl, 20 mM MnCl<sub>2</sub>, 0.02% NaN<sub>3</sub>, 5 mM UDP-GlcNAc, 100 mU/mg GnT-I, 60 mU/mg GnT-II. The reaction achieved 92% completion of the addition of bi-antennary  
5 GlcNAc moieties, with 8% mono-antennary GlcNAc moieties. Figure 143A shows the HPLC analysis of the released glycans, where peak "P3" represents the bi-antennary GlcNAc glycan. Figure 143B depicts the MALDI analysis of the released glycans with the structures of the glycans indicated beside the peak that they represent.

In order to further the reaction, an additional 20 mU/mg of GnT-II was added along  
10 with 1 mM UDP-GlcNAc, 5 mM MnCl<sub>2</sub>, 0.02% NaN<sub>3</sub>, and the mixture was incubated for 4 hours at 32°C. Greater than 99% of this reaction achieved completion of the bi-antennary GlcNAc glycan.

**GalT-1 Reaction.** The GalT-1 reaction was started immediately after the completion of the second GnT-II reaction. Enzyme and nucleotide sugar were added to the completed  
15 GnT-II reaction at concentrations of 0.5 U/mg GalT-1 and 3 mM UDP-Gal.

When the GalT-1 reaction was performed on a small scale, with about 100 µg EPO per reaction, approximately 95% of the reaction produced EPO with bi-antennary terminal galactose moiety. Figure 144A depicts the HPLC analysis of the released glycans where  
20 peak "P2" is the bi-antennary glycan with terminal galactose moieties (85% of the glycans), and peak "P1" is the bi-antennary glycan without the terminal galactose moieties (15% of the glycans).

The GalT-1 reaction was also performed on a large scale with about 16 mg of EPO per reaction. Figure 144B depicts the HPLC analysis of the release glycans from the large  
25 scale GalT-1 reaction, where peak "P2" is the bi-antennary glycan with terminal galactose moieties, and peak "P1" is the bi-antennary glycan without the terminal galactose moieties.



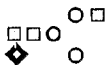
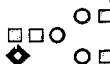
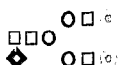
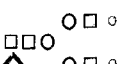
**Superdex 75 Purification.** EPO was then purified from the enzyme protein contaminants and nucleotide sugars using a 1.6 cm x 60 cm Superdex-75 gel filtration chromatography (Amersham Biosciences, Arlington Heights, IL) in PBS containing 0.02% Tween 20 after the GnT-1/GalT1 reaction. Figure 145 depicts the chromatogram of the  
30 Superdex 75 gel filtration, where peak 2 is EPO with bi-antennary glycans with terminal galactose moieties. Figure 146 shows SDS-PAGE analysis of the products of each

remodeling step indicating the increase in the molecular weight of EPO with each remodeling step.

**ST3Gal3 Reaction.** The ST3Gal3 reaction was incubated at 32°C for 24 hours. The reaction contained 0.5 mg/mL EPO, 100 mM Tris-Cl pH 7.2, 150 mM NaCl, 0.02% NaN<sub>3</sub>, 100 mU/mg ST3Gal3, and 0.5 mM CMP-SA, 0.5 mM CMP-SA-PEG (1 kDa), or 0.5 mM CMP-SA-PEG (10 kDa). Figure 147 shows the results of SDS-PAGE analysis of EPO before and after the ST3Gal3 reaction. Based on this SDS-PAGE analysis, bi-antennary EPO containing terminal Gal can no longer be visually detected after each ST3Gal3 reaction. All sialylated EPO variants show an increase in size compared to non-sialylated EPO at the start of the reaction.

**Superdex 200 Purification.** EPO was purified from the contaminants of the ST3Gal3 reactions by a 1.6 cm x 60 cm Superdex-200 gel filtration chromatography (Amersham Biosciences, Arlington Heights, IL) in PBS containing 0.02% Tween-20. Table 23 summarizes the distribution of glycan structures at each remodeling step.

**Table 23.** Summary of glycan structures on EPO after each remodeling step.

Glycan	Starting Material	After GnT-I and GnT-II	After 2nd GnT-II	After GalT-1	After ST
	0.5%				
	98.0%				
	1.0%	8.0%	0.5%	0.5%	0.5%
	0.5%	92.0%	99.5%	15.5%	15.5%
				84.0%	2.0%
					82.0%

Diamonds represent fucose, and squares represent GlcNAc, circles represent mannose, open circles represent galactose.

### Tri-antennary Branching

Several reactions were performed to accomplish the tri-antennary branching of EPO. Briefly, the first reaction combined the GnT-I and GnT-II reactions to add a GlcNAc moiety to the two outer tri-mannosyl core branches of the glycan. The second reaction, GnT-V  
5 reaction, adds a second GlcNAc moiety to one of the two outer trimannosyl core branches so that there are now three GlcNAc moieties. The third reaction, GalT-1 reaction, adds a galactose moiety to each terminal GlcNAc moiety. The EPO products were then separated by Superdex 75 chromatography. The tri-antennary branching was further extended with the ST3Gal3 reaction to add either a 2,3-SA moiety or a 2,6-SA moiety, and capped with a 2,3-  
10 SA moiety. Final purification was accomplished using Superdex 75 chromatography.

**GnT-I/GnT-II Reaction.** The GnT-I and GnT-II reactions were combined and incubated at 32°C for 24 hours. The reaction contained 1 mg/mL EPO, 100 mM MES pH 6.5, 150 mM NaCl, 20 mM MnCl<sub>2</sub>, 0.02% NaN<sub>3</sub>, 5 mM UDP GlcNAc, 50 mU/mg GnT-I and 41 mU/mg GnT-II. The reaction achieved 97% completion of the addition of the bi-  
15 antennary GlcNAc moiety, with 3% tri-mannosyl core remaining. Figure 148 depicts the HPLC analysis of the glycans released from EPO after the GnT-I/GnT-II reaction.

**GnT-V Reaction.** The GnT-V reaction containing 100 mM MES pH 6.5, 5 mM UDP-GlcNAc, 5 mM MnCl<sub>2</sub>, 0.02% NaN<sub>3</sub>, 10 mU/mg GnT-V and 1 mg/mL EPO, was incubated at 32°C for 24 hours. This reaction adds a GlcNAc moiety to an outer mannose  
20 moiety already containing a GlcNAc moiety. Figure 149 depicts the HPLC analysis of the glycans released from EPO after the GnT-V reaction. Approximately 92% the glycans released from EPO were the desired product, tri-antennary branched EPO with terminal GlcNAc moieties, based on glycan and MALDI analysis. The remaining 8% of the glycans were bi-antennary branched structures containing terminal GlcNAc moieties.

**GalT-1 Reaction.** The GalT-1 reaction containing 100 mM Tris pH 7.2, 150 mM NaCl, 5 mM UDP Gal, 100 mU/mg GalT-1, 5 mM MnCl<sub>2</sub>, 0.02% NaN<sub>3</sub> and 1 mg/mL EPO was incubated at 32°C for 24 hours. Figure 150 depicts the HPLC analysis of the glycans released from EPO after this reaction. Glycan and MALDI analysis indicates that 97% of the released glycans had terminal galactose moieties on the tri-antennary branched structures.  
25  
30 The remaining 3% was a bi-antennary structure containing a terminal galactose.

**Superdex 75 Purification.** After the GnT-I/GalT1 reaction, EPO was purified from the enzyme protein contaminants and nucleotide sugars using a 1.6 cm x 60 cm Superdex-75 gel filtration chromatography (Amersham Biosciences, Arlington Heights, IL) in PBS containing 0.02% Tween 20. The purified material was divided into two batches to produce the tri-antennary glycan with terminal 2,6-SA moieties and the tri-antennary glycan with terminal 2,6-SA moieties capped with 2,6-SA moieties.

**ST3Gal3 Reaction.** The ST3Gal3 reaction was incubated at 32°C for 24 hours. The reaction contained 1 mg/mL galactosylated EPO, 100 mM Tris-Cl pH 7.2, 150 mM NaCl, 0.02% NaN<sub>3</sub>, 50 mU/mg ST3Gal3, and 3 mM CMP-SA. Figure 151 depicts the HPLC analysis of glycans released from EPO after this step. Based on glycan and MALDI analysis, approximately 80% of the released glycans were tri-antennary branched structures with terminal 2,3-SA moieties. The remaining 20% of the released glycans were bi-antennary structures with terminal 2,3-SA moieties.

**ST6Gal1 sialylation Reaction following the ST3Gal3 Reaction.** The ST6Gal1 reaction was incubated at 32°C for 24 hours. The reaction contained 1 mg/mL sialylated galactosylated EPO, 100 mM Tris-Cl pH 7.2, 150 mM NaCl, 0.02% NaN<sub>3</sub>, 50 mU/mg ST6Gal1, and 3 mM CMP-SA. Figure 152 depicts the results of HPLC analysis of the glycans released from EPO after the ST6Gal1 reaction. Based on glycan and MALDI analysis, approximately 80% of the tri-antennary branched glycans contained terminal 2,3-SA moieties. The remaining 20% of the glycans were bi-antennary with terminal 2,3-SA moieties.

**Superdex 75 Purification.** EPO was purified from the contaminants of the ST3Gal3 reactions by a 1.6 cm x 60 cm Superdex-75 gel filtration chromatography (Amersham Biosciences, Arlington Heights, IL) in PBS containing 0.02% Tween-20.

**Bioassay of Tri-antennary and Bi-antennary Sialylated or PEGylated EPO.** The activity of the tri-antennary and bi-antennary sialylated EPO glycoforms, and the PEG 10 kDa and 1 kDa bi-antennary glycoforms were assayed using the TF-1 cell line and the MTT viability test, as described above. Figure 153 depicts the results of the MTT cell proliferation assay. At 2 µg/ml EDP, the bi-antennary sialylated EPO had nearly the activity of the control Epogen, while the tri-antennary sialylated EPO had significantly less activity.